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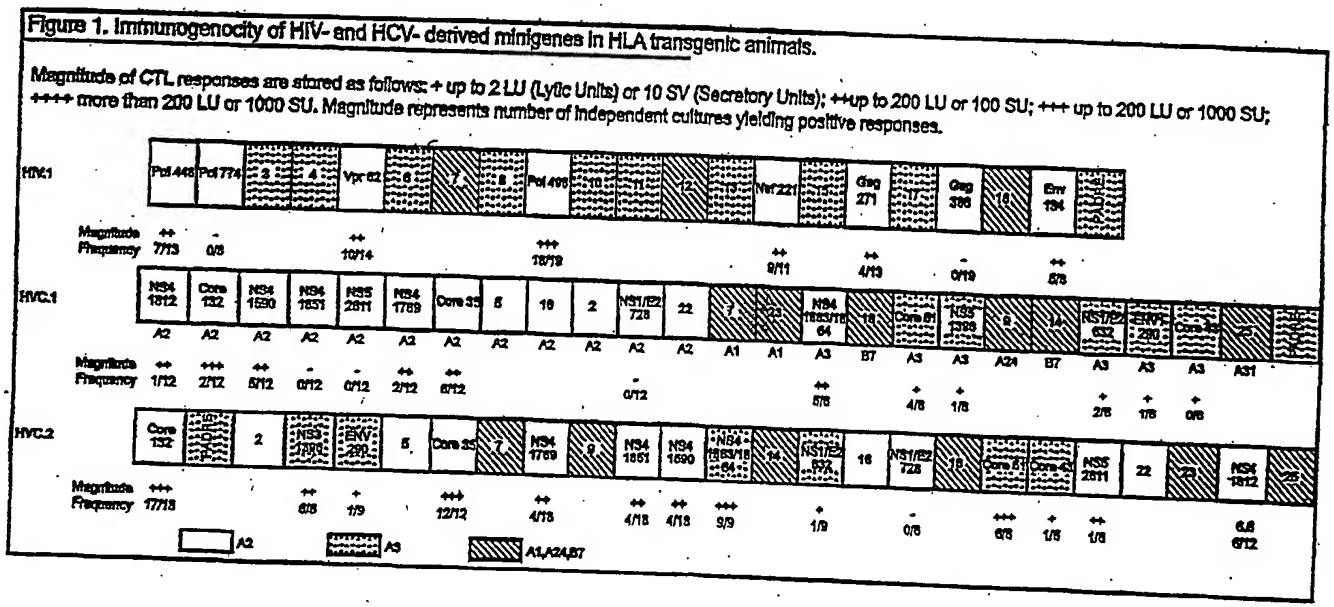
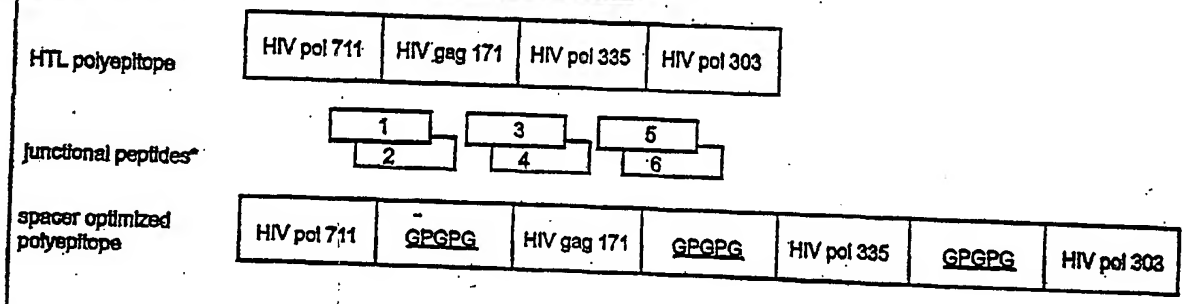


Figure 1. Immunogenocity of HIV- and HCV- derived minigenes in HLA transgenic animals.
Magnitude of CTL responses are stored as follows: + up to 2 LU (Lytic Units) or 10 SV (Secretory Units); ++up to 200 LU or 100 SU; +++ up to 200 LU or 1000 SU; ++++ more than 200 LU or 1000 SU. Magnitude represents number of independent cultures yielding positive responses.
HIV.1
Pol 448
Pol 774
3
4
Vpr 62
6
7
8
Pol 499
10
11
12
13
Nef 221
Gag 271
Gag 386
16
Env 194
Magnitude
Frequency
7/13
0/8
10/14
18/19
9/11
4/13
0/19
5/8
HVC.1
NS4 1812
Core 132
NS4 1630
NS4 1851
NS5 2911
NS4 1769
Core 35
5
19
2
NS1/E2 728
22
7
23
NS4 1883/18 64
18
Core 81
NS5 1399
9
14
NS1/E2 632
E1/P7 290
Core 43
25
A2
A1
A3
B7
A24
A31
Magnitude
Frequency
1/12
2/12
5/12
0/12
0/12
2/12
6/12
0/12
5/8
4/8
1/8
2/8
1/8
0/8
HVC.2
Core 132
NS3 1806
2
NS3 1806
ENV 290
5
Core 35
7
NS4 1769
9
NS4 1851
NS4 1630
NS4 1883/18 64
14
NS1/E2 632
16
NS1/E2 728
18
Core 81
Core 43
NS5 2911
22
23
NS4 1812
25
Magnitude
Frequency
17/18
6/8
1/9
12/12
4/18
4/18
4/18
9/9
1/9
0/8
6/8
1/8
1/8
6,8
6/12
A2
A3
A1,A24,B7

FIG. 1

Figure 2a. Synthetic polypeptides encoding HIV-derived HTL epitopes



*junction peptides comprise either 10 amino acids from the N-terminal epitope and 5 amino acids from the C-terminal epitope or 5 amino acids from the N-terminal epitope and 10 amino acids from the C-terminal epitope.

FIG. 2a

Figure 2b. Proliferative responses to synthetic polypeptides encoding HIV-derived HTL

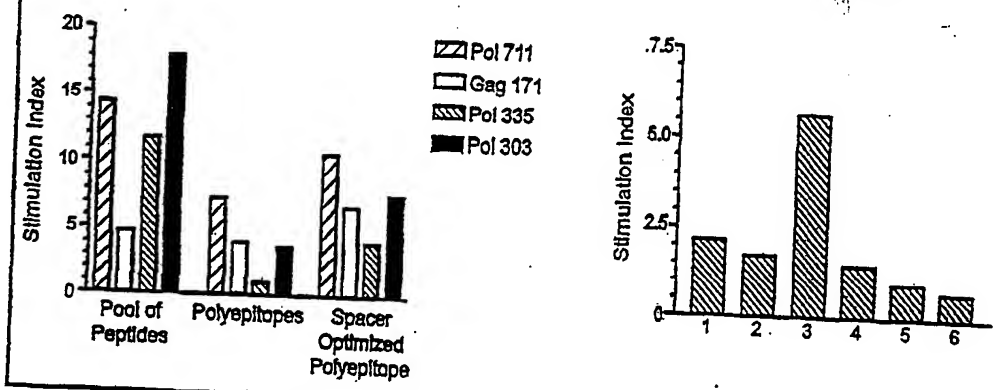
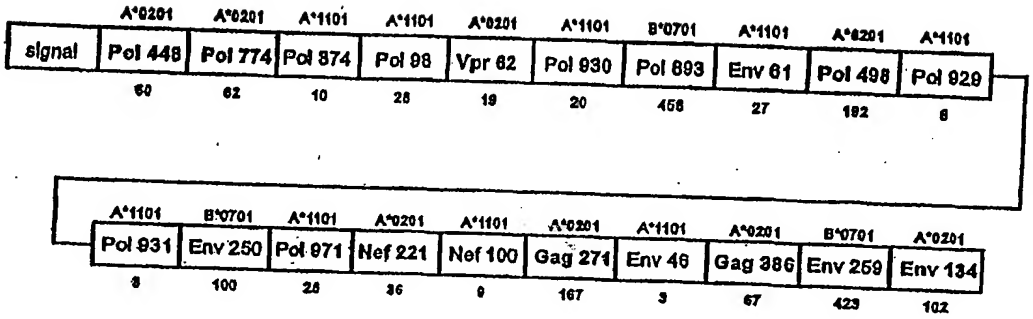


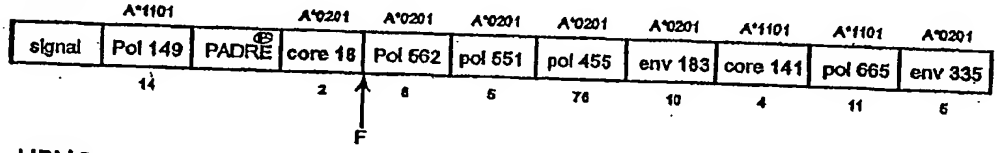
FIG. 2b

a : HIV-FT

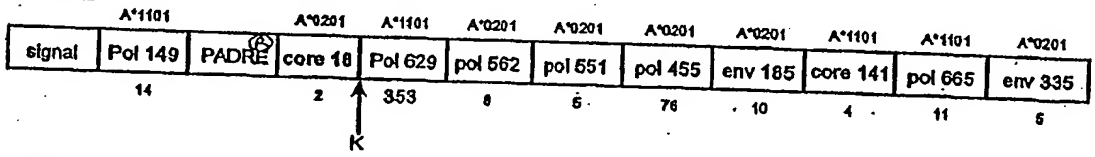


b : HBV-specific multiepitope constructs

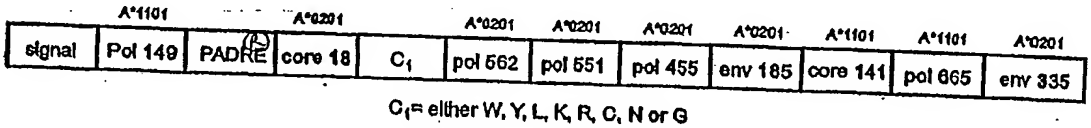
HBV.1



HBV.2



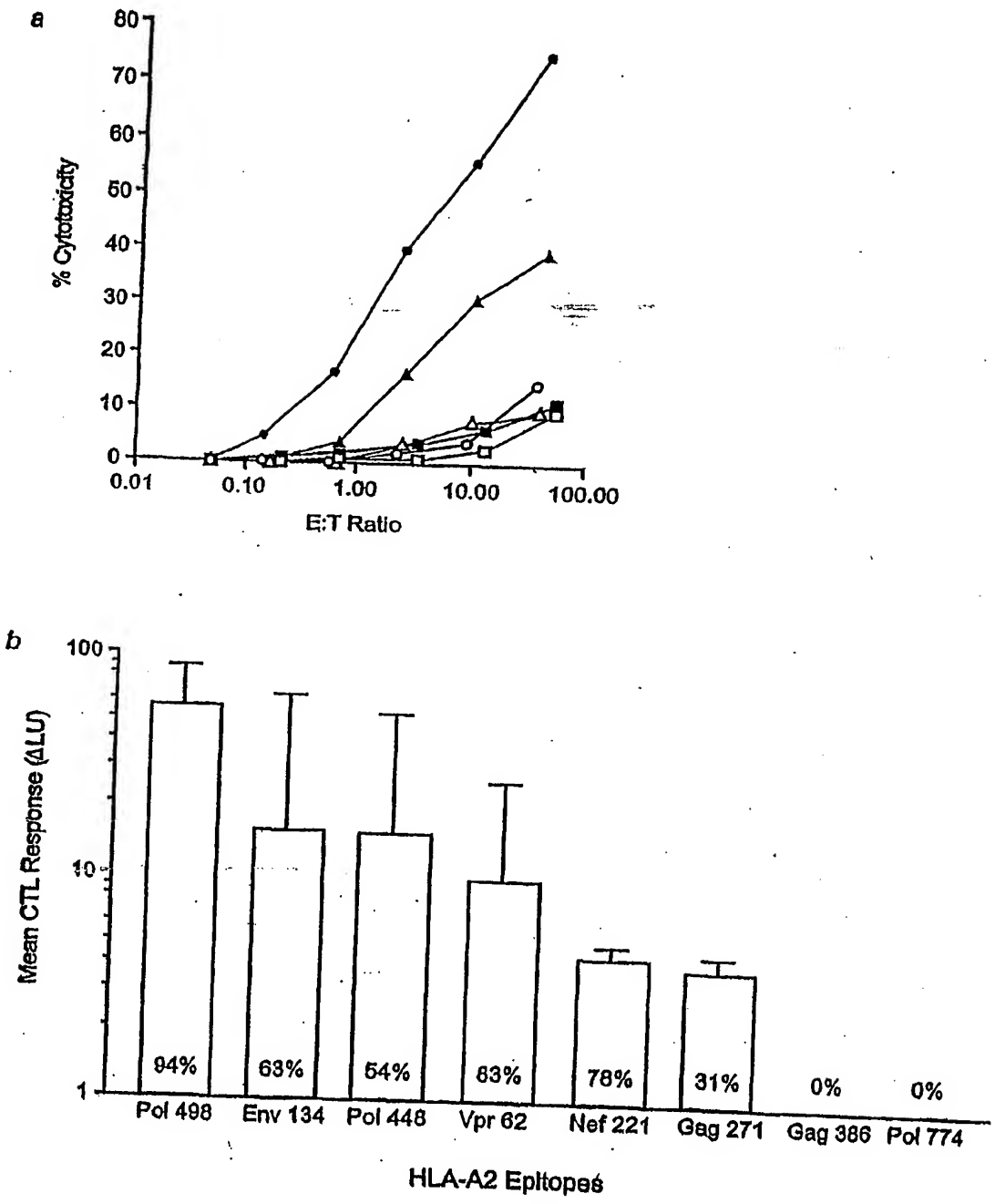
HBV.1X



C_1= either W, Y, L, K, R, C, N or G

FIG. 3

Figure 4


a
% Cytotoxicity
E:T Ratio
b
Mean CTL Response (ΔLU)
94%
63%
54%
63%
78%
31%
0%
0%
Pol 498
Env 134
Pol 448
Vpr 62
Nef 221
Gag 271
Gag 386
Pol 774
HLA-A2 Epitopes

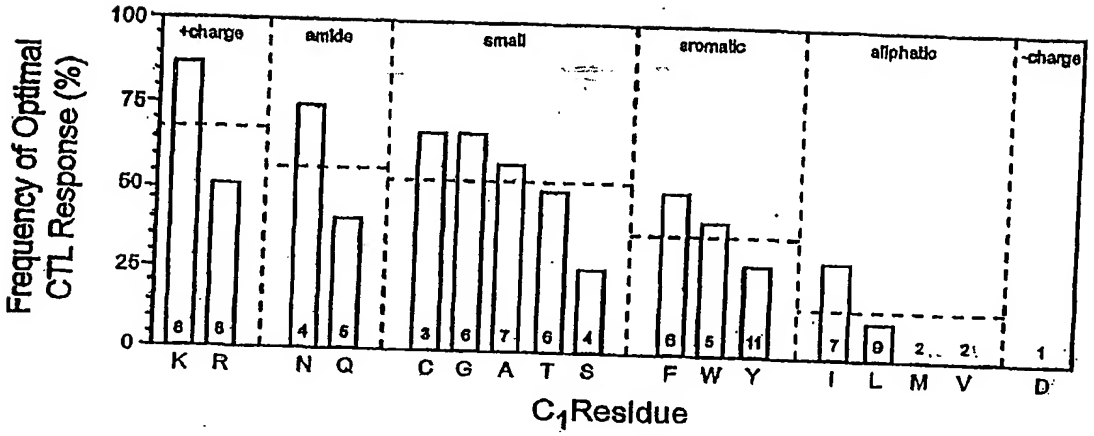

Frequency of Optimal CTL Response (%)
100
75
50
25
0
+charge
amide
small
aromatic
aliphatic
-charge
6
6
4
5
3
6
7
6
4
6
5
11
7
9
2
2
1
K R N Q C G A T S F W Y I L M V D
C1Residue

FIG. 5

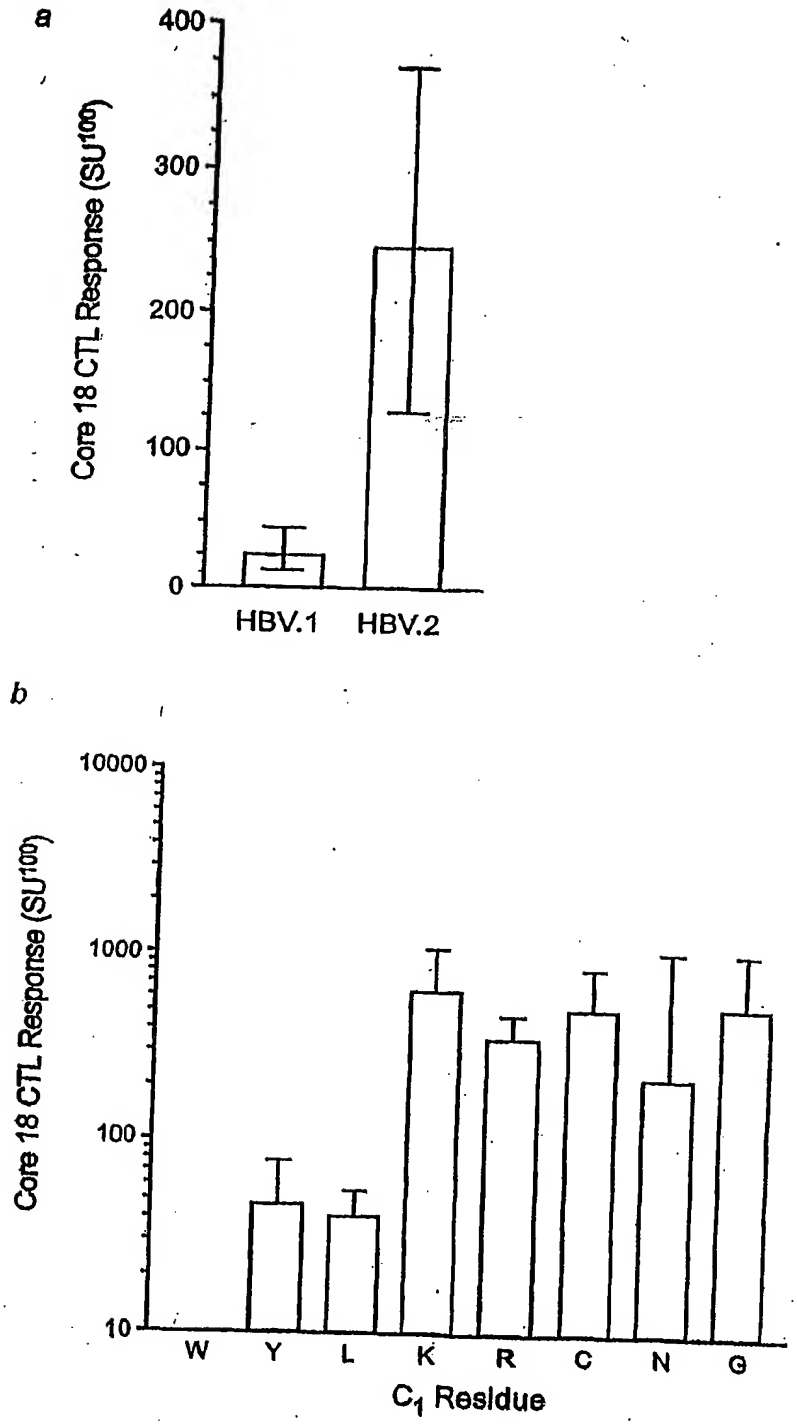

a
400
300
200
100
0
Core 18 CTL Response (SU100)
HBV.1
HBV.2
b
10000
1000
100
10
Core 18 CTL Response (SU100)
W
Y
L
K
R
C
N
G
C1 Residue

FIG. 6

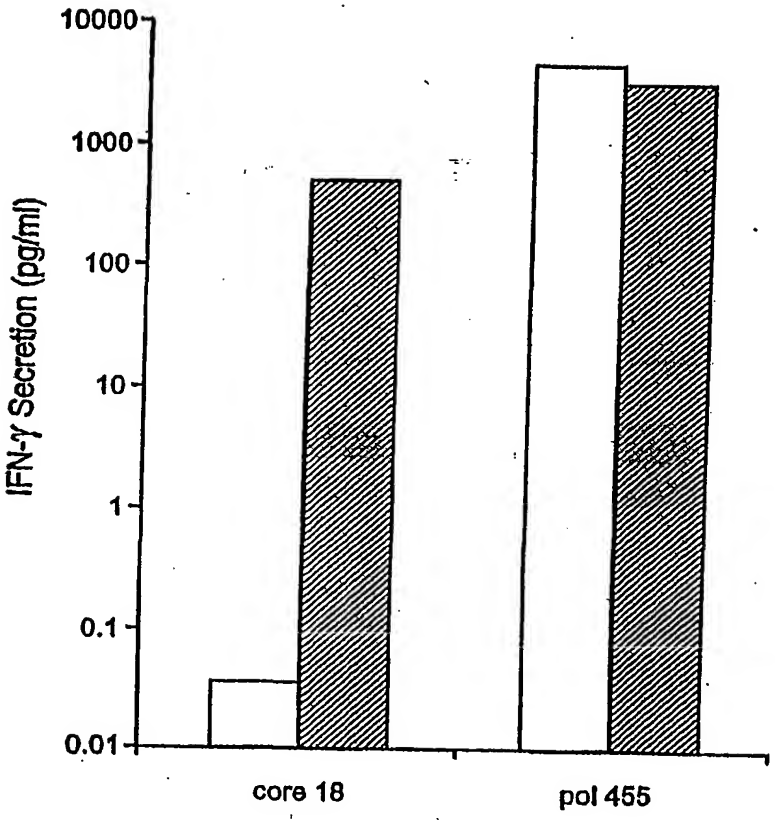


FIG. 7

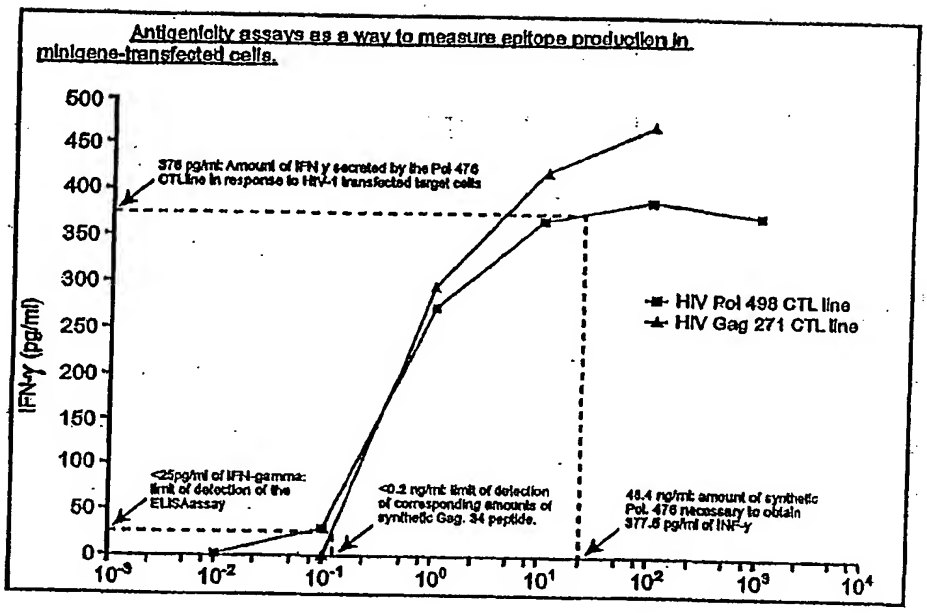
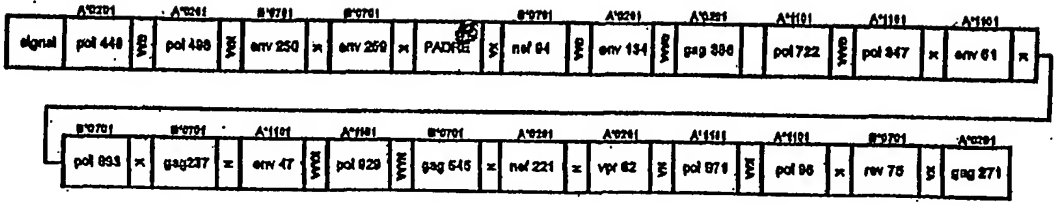
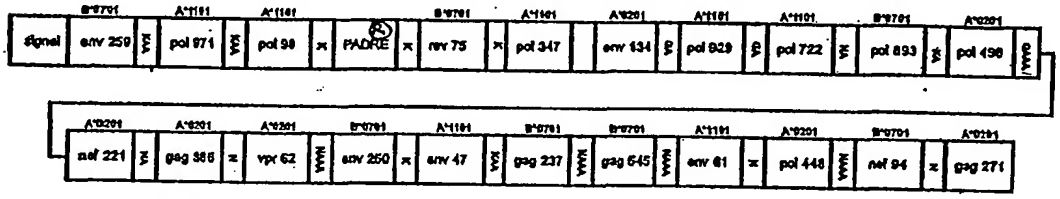

Antigenicity assays as a way to measure epitope production in minigene-transfected cells.
IFN-γ (pg/ml)
500
450
400
350
300
250
200
150
100
50
0
376 pg/ml: Amount of IFN γ secreted by the Pol 476 CTLline in response to HIV-1 transfected target cells
HIV Pol 498 CTL line
HIV Gag 271 CTL line
<25pg/ml of IFN-gamma: limit of detection of the ELISAassay
<0.2 ng/ml: limit of detection of corresponding amounts of synthetic Gag. 34 peptide.
48.4 ng/ml: amount of synthetic Pol. 476 necessary to obtain 377.6 pg/ml of INF-γ
10-3
10-2
10-1
100
101
102
103
104

FIG. 8

HIV-TT



HIV-DG



HIV-TC

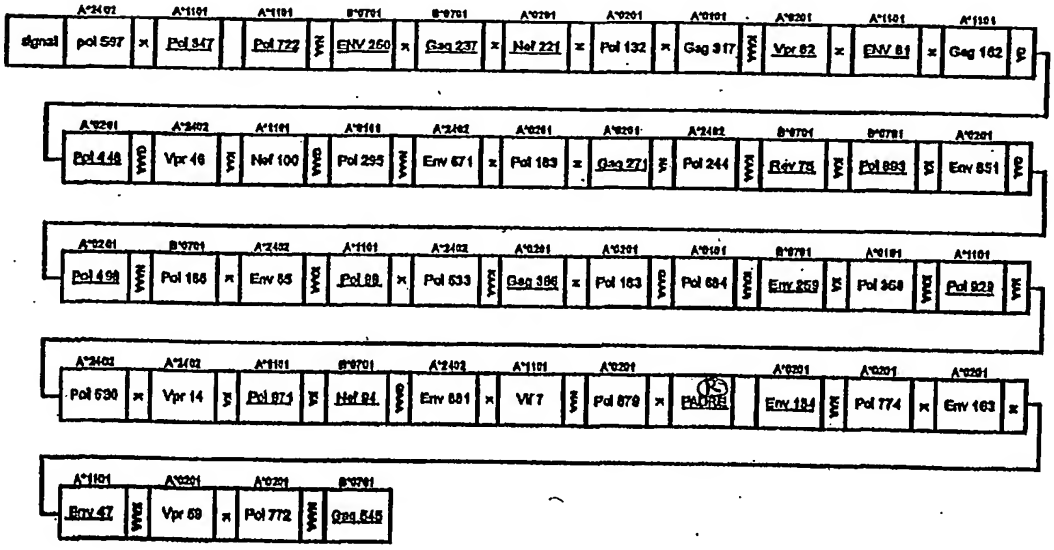


FIG. 9

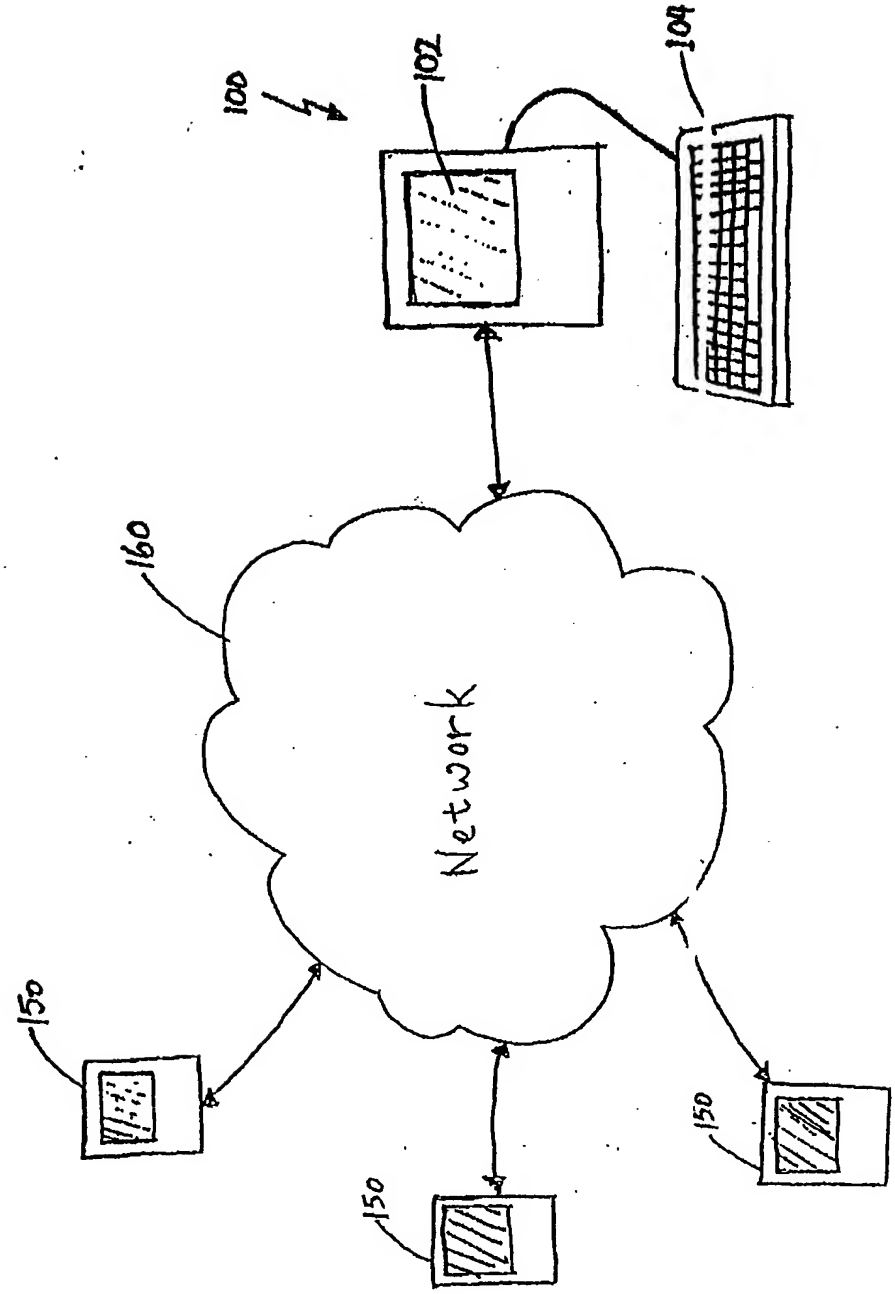


FIGURE 10

200

Sequence	Length	Code
VLAEAMSQV	9	A
ILKEPVHGV	9	B
TLNFPISPI	9	C
SLLNATDIAV	10	D
QMAVFIHNFK	10	E
VTVYYGVPVWK	11	F
FPVRPQVPL	9	G
YPLASLRSLF	10	H
VIYQYMDDLY	10	I
IYQEPFKNL	9	J
IWGCSGKLI	9	K

202

AA	Ct-1 ranking	N-1 ranking
K	2.20	0.64
C	2.00	1.00
N	2.00	0.00
G	1.80	1.33
T	1.50	0.00
A	1.33	1.21
F	1.33	1.00
S	1.33	0.00
W	1.20	0.00
Q	1.20	0.00
R	1.17	1.57
M	1.00	0.00
Y	1.00	0.75
I	0.86	0.50
L	0.75	2.20
V	0.00	1.19
D	0.00	0.00
H	0.00	0.00
E	0.00	0.00
P	0.00	0.00

204

Motif Specification

XXXX(FY)XX(LIMV)
XXXX(FY)XXX(LIMV)
XXXXNXXX(LIMV)
XXXXNXXXX(LIMV)
X(LM)XXXXXXV
X(LM)XXXXXXXV
X(LMVT)XXXXXX(KRY)
X(LMVT)XXXXXXX(KRY)
XPXXXXXX(LIMVF)
XPXXXXXXX(LIMVF)

206

FIGURE 11A

MaxInsertions=(enter value here) 208

OutputToScreen=yes/no 210

OutputToFile=yes/no 212

MinimumAccepted=(enter value here) 214

MaxDuplicateFunctionValues=(enter value here) 216

MaxSearchTime (min.)=(enter value here) 218

Exhaustive=yes/no 220

NumStochasticProbes=(enter value here) 222

MaxHitsPerProbe=(enter value here) 224

RandomProbeStart=yes/no 226

FIGURE 11B

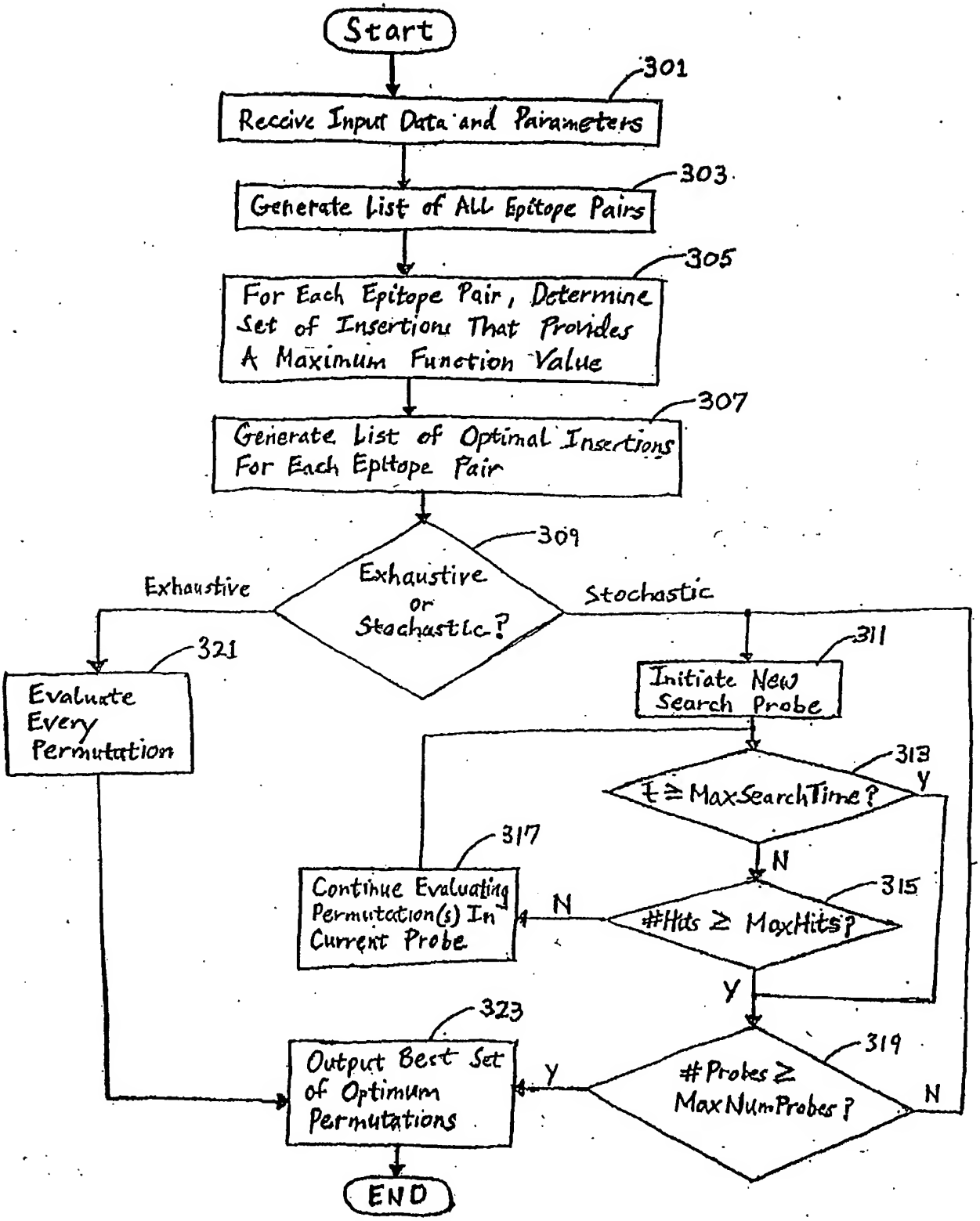

Start
301
Receive Input Data and Parameters
303
Generate List of ALL Epitope Pairs
305
For Each Epitope Pair, Determine Set of Insertions That Provides A Maximum Function Value
307
Generate List of Optimal Insertions For Each Epitope Pair
309
Exhaustive or Stochastic?
Exhaustive
Stochastic
321
Evaluate Every Permutation
311
Initiate New Search Probe
313
t ≥ MaxSearchTime?
Y
N
315
#Hits ≥ MaxHits?
N
317
Continue Evaluating Permutation(s) In Current Probe
Y
319
Probes ≥ MaxNumProbes?
Y
N
323
Output Best Set of Optimum Permutations
END

FIGURE 12

Junctional Analyzer run on Saturday, February 26, 2000 09:06:23 pm.

The following non-zero AA weights will be used.

AA	N-1 ranking	C+1 ranking
A	1.21	1.33
C	1.00	2.00
F	1.00	1.83
G	1.33	1.80
I	0.50	0.86
K	0.64	2.20
L	2.20	0.75
M	0.00	1.00
N	0.00	2.00
Q	0.00	1.20
R	1.57	1.17
S	0.00	1.33
T	0.00	1.50
V	1.19	0.00
W	0.00	1.20
Y	0.75	1.00

204

The following 10 motif specifications will be used to search for junctionals.

Count	Motif Specification
1	XXXX(FY)XX(LIMV)
2	XXXX(FY)XXX(LIMV)
3	XXXXNXXX(LIMV)
4	XXXXNXXXX(LIMV)
5	X(LM)XXXXXXV
6	X(LM)XXXXXXV
7	X(LMVT)XXXXXX(KRY)
8	X(LMVT)XXXXXXX(KRY)
9	XPXXXXXX(LIMVF)
10	XPXXXXXXX(LIMVF)

206

Code	Peptide	Length
A	VLAEAMSQV	9
B	ILKEPVHGV	9
C	TLNFPISPI	9
D	SLLNATDIAV	10
E	QMAVFIHNFK	10
F	VTVYYGVPVWK	11
G	FPVRPQVPL	9
H	YPLASLRSLF	10
I	VIYQYMDDLY	10
J	IYQEPFKNL	9
K	IWGCSGKLI	9

202

MaxInsertions = 4 (208)

FIGURE 13A

OutputToScreen = No

OutputToFile = Yes

MinimumValueAccepted = 0

MaxDuplicateFunctionValues = 50

SearchTime = 5

NumStochasticProbes = 10

MaxHitsPerProbe = 25

RandomProbeStart = Yes

Col. 1 Code 1	Col. 2 I1	Col. 3 I2	Col. 4 I3	Col. 5 I4	Col. 6 Code 2	Col. 7 C	Col. 8 N	Col. 9 C+N	Col. 10 J	Col. 11 MaxFunc.
A	C	A		L	B	2.00	2.20	4.40	0	8.80
A	C			L	C	2.00	2.20	4.40	0	8.80
A	C			L	D	2.00	2.20	4.40	0	8.80
A	C			L	E	2.00	2.20	4.40	0	8.80
A	C			R	F	2.00	1.57	3.14	2	1.57
A	C			R	G	2.00	1.57	3.14	1	3.14
A	C			R	H	2.00	1.57	3.14	0	6.28
A	G				I	1.80	1.33	2.39	1	2.39
A	C	A	A	G	J	2.00	1.33	2.66	0	5.32
A	C			R	K	2.00	1.57	3.14	0	6.28
B	C	A	A	G	A	2.00	1.33	2.66	0	5.32
B	C	A		R	C	2.00	1.57	3.14	0	6.28
B	C	A		R	D	2.00	1.57	3.14	0	6.28
B	C	A		R	E	2.00	1.57	3.14	0	6.28
B	C	A	A	G	F	2.00	1.33	2.66	1	2.66
B	C			R	G	2.00	1.57	3.14	1	3.14
B	C			R	H	2.00	1.57	3.14	0	6.28
B	C	A	A	G	I	2.00	1.33	2.66	1	2.66
B	C	A	A	G	J	2.00	1.33	2.66	0	5.32
B	C	A	A	G	K	2.00	1.33	2.66	0	5.32
C	C	A		R	A	2.00	1.57	3.14	1	3.14
C	C	A		R	B	2.00	1.57	3.14	1	3.14
C	C			L	D	2.00	2.20	4.40	1	4.40
C	C	A		R	E	2.00	1.57	3.14	1	3.14
C	C			R	F	2.00	1.57	3.14	1	3.14
C	C			R	G	2.00	1.57	3.14	1	3.14
C	C			R	H	2.00	1.57	3.14	1	3.14
C	C	A		R	I	2.00	1.57	3.14	0	6.28
C	C	A	A	R	J	2.00	1.57	3.14	1	3.14
C	C	A	A	R	K	2.00	1.57	3.14	0	6.28

FIGURE 13B

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
D	C			L	A	2.00	2.20	4.40	0	8.80
D	C			L	B	2.00	2.20	4.40	0	8.80
D	C			L	C	2.00	2.20	4.40	0	8.80
D	C			L	E	2.00	2.20	4.40	0	8.80
D	G				F	1.80	1.33	2.89	0	4.79
D	C			R	G	2.00	1.57	3.14	0	6.28
D	C	A	A	G	H	2.00	1.33	2.66	0	5.32
D	C			L	I	2.00	2.20	4.40	1	4.40
D	C	A		G	J	2.00	1.33	2.66	0	5.32
D	C			R	K	2.00	1.57	3.14	0	6.28
E	C	A	A	L	A	2.00	2.20	4.40	0	8.80
E	C	A	A	L	B	2.00	2.20	4.40	0	8.80
E	C	A	A	L	C	2.00	2.20	4.40	0	8.80
E	C	A	A	L	D	2.00	2.20	4.40	0	8.80
E	C	A		R	F	2.00	1.57	3.14	0	6.28
E	C	A		R	G	2.00	1.57	3.14	0	6.28
E	C	A		R	H	2.00	1.57	3.14	0	6.28
E	C	A	A	L	I	2.00	2.20	4.40	0	8.80
E	C	A		R	J	2.00	1.57	3.14	0	6.28
E	C	A		R	K	2.00	1.57	3.14	0	6.28
F	K			L	A	2.20	2.20	4.84	1	4.84
F	K	A	A	G	B	2.20	1.33	2.93	1	2.93
F	K	A	A	G	C	2.20	1.33	2.93	0	5.85
F	K	A	A	G	D	2.20	1.33	2.93	0	5.85
F	K	A	A	G	E	2.20	1.33	2.93	0	5.85
F	K	A		G	G	2.20	1.33	2.93	1	2.93
F	K	A		G	H	2.20	1.33	2.93	1	2.93
F	K	A	A	G	I	2.20	1.33	2.93	1	2.93
F	K			R	J	2.20	1.57	3.45	1	3.45
F	K			R	K	2.20	1.57	3.45	0	6.91
G	C	A		R	A	2.00	1.57	3.14	1	3.14
G	C	A		R	B	2.00	1.57	3.14	2	1.57
G	C	A		R	C	2.00	1.57	3.14	1	3.14
G	C			L	D	2.00	2.20	4.40	1	4.40
G	C	A		R	E	2.00	1.57	3.14	2	1.57
G	C			L	F	2.00	2.20	4.40	4	1.10
G	C			G	H	2.00	1.33	2.66	0	5.32
G	C	A	A	R	I	2.00	1.57	3.14	2	1.57
G	C	A	A	R	J	2.00	1.57	3.14	1	3.14
G	C	A	A	R	K	2.00	1.57	3.14	0	6.28
H	C	A	A	G	A	2.00	1.33	2.66	0	5.32
H	C	A	A	G	B	2.00	1.33	2.66	1	2.66
H	C	A		G	C	2.00	1.33	2.66	0	5.32
H	C	A		G	D	2.00	1.33	2.66	0	5.32
H	C	A	A	G	E	2.00	1.33	2.66	0	5.32
H	C	A	A	G	F	2.00	1.33	2.66	1	2.66
H	C			R	G	2.00	1.57	3.14	1	3.14
H	C	A	A	G	I	2.00	1.33	2.66	1	2.66
H	C	A		G	J	2.00	1.33	2.66	1	2.66
H	C	A	A	G	K	2.00	1.33	2.66	0	5.32

FIGURE 13C

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
I	K	A	A	G	A	2.20	1.33	2.93	0	5.85
I	K	A	A	G	B	2.20	1.33	2.93	1	2.93
I	K	A		G	C	2.20	1.33	2.93	0	5.85
I	K	A		G	D	2.20	1.33	2.93	0	5.85
I	K	A	A	G	E	2.20	1.33	2.93	0	5.85
I	K	A	A	G	F	2.20	1.33	2.93	1	2.93
I	K			R	G	2.20	1.57	3.45	1	3.45
I	K	A	A	G	H	2.20	1.33	2.93	0	5.85
I	K	A		G	J	2.20	1.33	2.93	1	2.93
I	K	A	A	G	K	2.20	1.33	2.93	0	5.85
J	K	A	A	R	A	2.20	1.57	3.45	0	6.91
J	K	A	A	R	B	2.20	1.57	3.45	1	3.45
J	K	A		R	C	2.20	1.57	3.45	0	6.91
J	K	A		R	D	2.20	1.57	3.45	0	6.91
J	K	A		R	E	2.20	1.57	3.45	1	3.45
J	K	A	A	R	F	2.20	1.57	3.45	2	1.73
J	K			R	G	2.20	1.57	3.45	1	3.45
J	K			R	H	2.20	1.57	3.45	0	6.91
J	K	A	A	R	I	2.20	1.57	3.45	1	3.45
J	K	A	A	R	K	2.20	1.57	3.45	0	6.91
K	K			L	A	2.20	2.20	4.84	0	9.68
K	K			L	B	2.20	2.20	4.84	0	9.68
K	K			L	C	2.20	2.20	4.84	0	9.68
K	K			L	D	2.20	2.20	4.84	0	9.68
K	K	A	A	L	E	2.20	2.20	4.84	0	9.68
K	K	A	A	R	F	2.20	1.57	3.45	1	3.45
K	G				G	1.80	1.33	2.39	0	4.79
K	K			R	H	2.20	1.57	3.45	0	6.91
K	K			L	I	2.20	2.20	4.84	1	4.84
K	K			R	J	2.20	1.57	3.45	0	6.91

Junctional Analyzer took 142.77 seconds.

FIGURE 13D

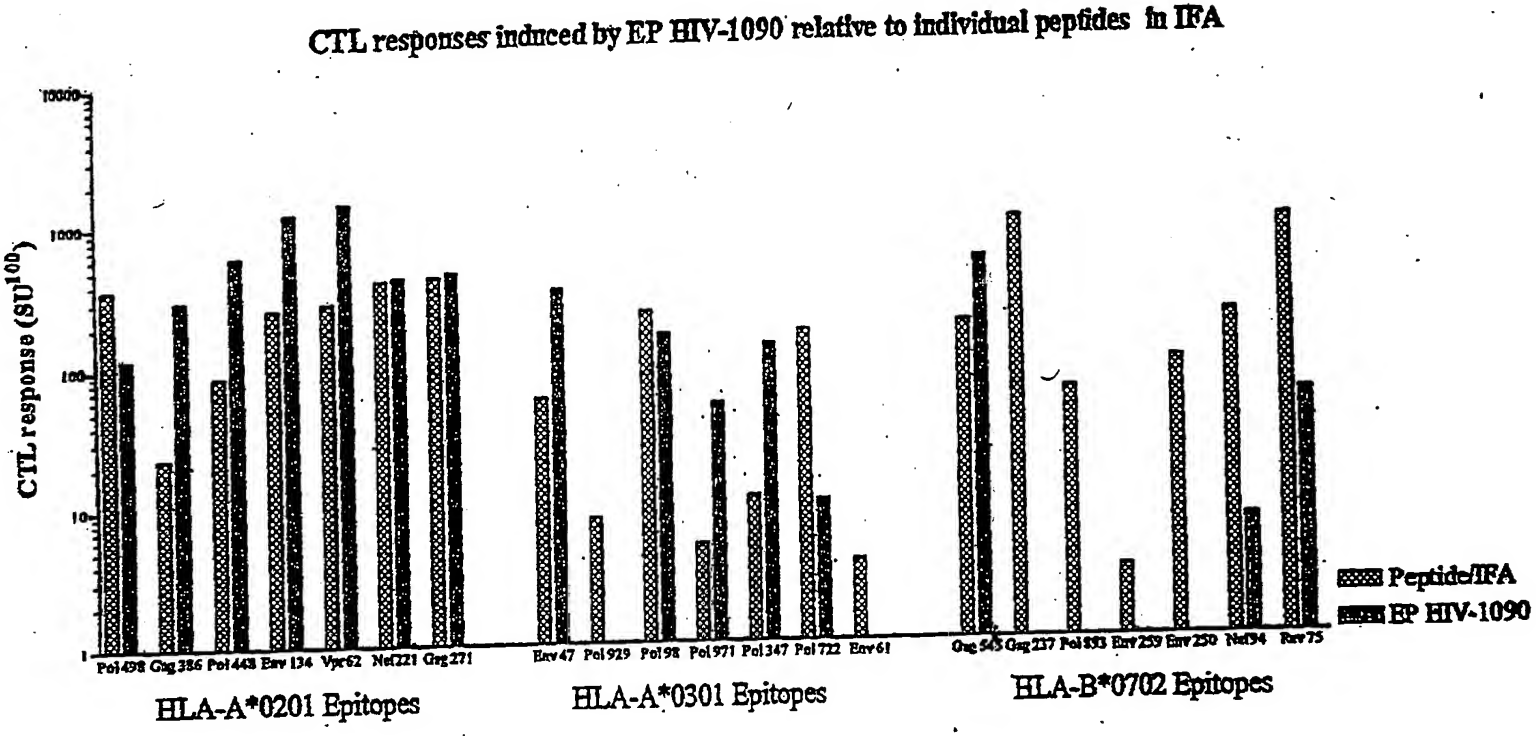

CTL responses induced by EP HIV-1090 relative to individual peptides in IFA
CTL response (SU/10^6)
10000
1000
100
10
1
Pol 498 Gag 386 Pol 448 Env 134 Vpr 62 Nef 221 Gag 271
Env 47 Pol 929 Pol 98 Pol 971 Pol 347 Pol 722 Env 61
Gag 543 Gag 217 Pol 853 Env 259 Env 250 Nef 94 Rev 75
HLA-A*0201 Epitopes
HLA-A*0301 Epitopes
HLA-B*0702 Epitopes
Peptide/IFA
EP HIV-1090

FIGURE 14A

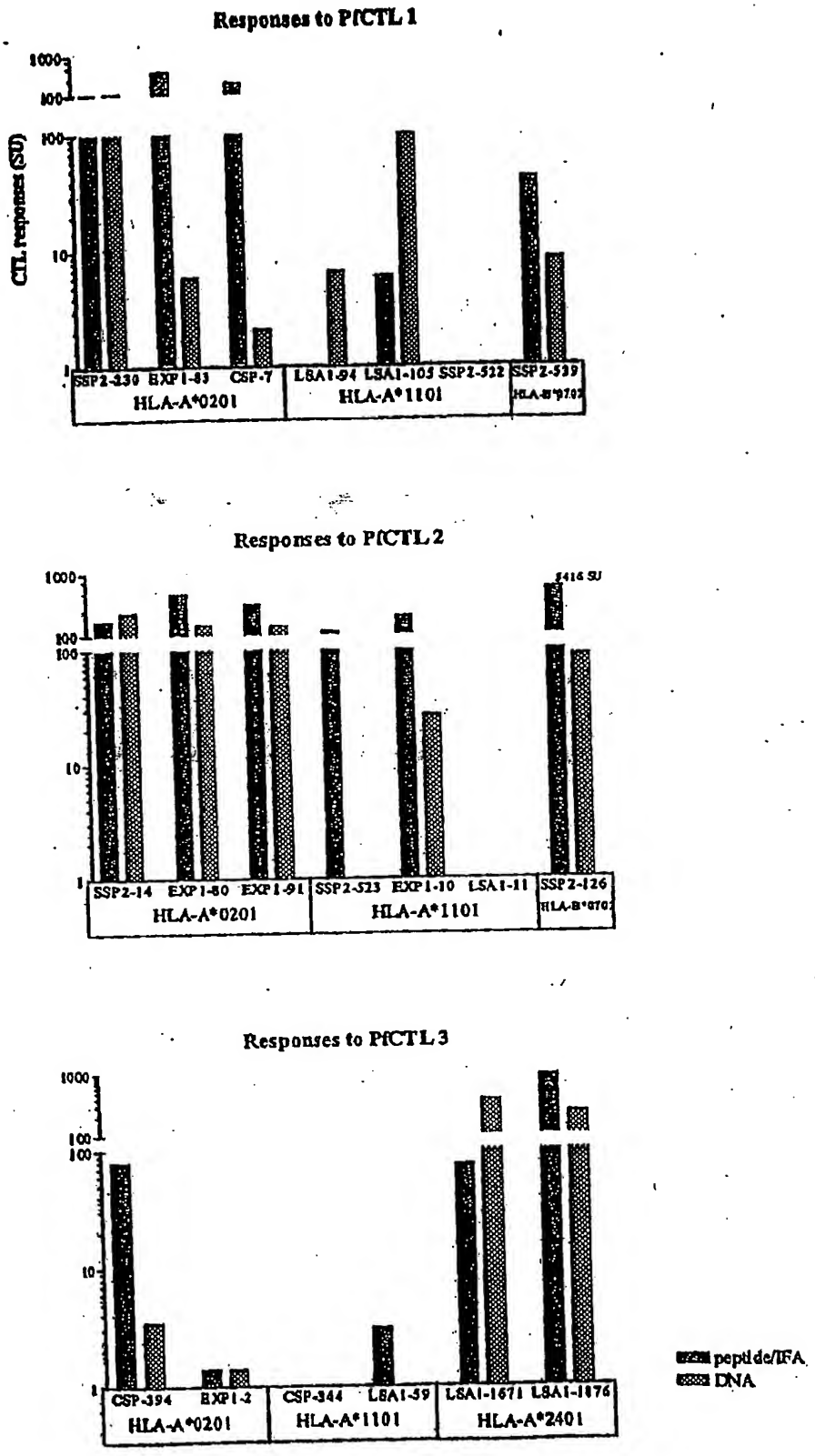

Responses to PfCTL 1
CTL response (SD)
1000
100
10
1
SSP2-330
EXP1-83
CSP-7
LSA1-94
LSA1-105
SSP2-522
SSP2-539
HLA-A*0201
HLA-A*1101
Responses to PfCTL 2
1000
100
10
1
SSP2-14
EXP1-80
EXP1-91
SSP2-523
EXP1-10
LSA1-11
SSP2-126
HLA-A*0201
HLA-A*1101
Responses to PfCTL 3
1000
100
10
1
CSP-394
EXP1-2
CSP-344
LSA1-59
LSA1-1671
LSA1-1876
HLA-A*0201
HLA-A*1101
HLA-A*2401
peptide/IFA
DNA

FIGURE 14B

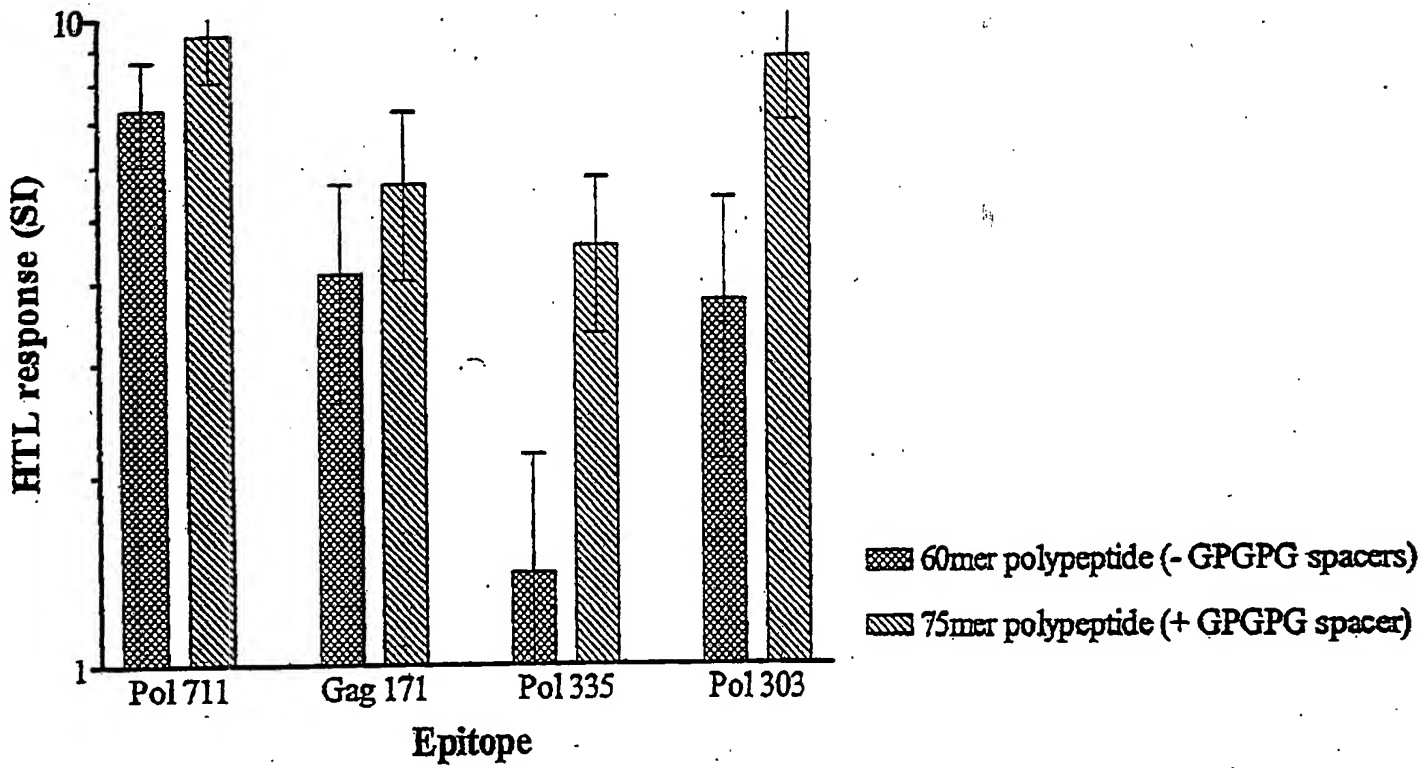

10
1
HTL response (SI)
Pol 711
Gag 171
Pol 335
Pol 303
Epitope
60mer polypeptide (- GPGPG spacers)
75mer polypeptide (+ GPGPG spacer)

FIGURE 15

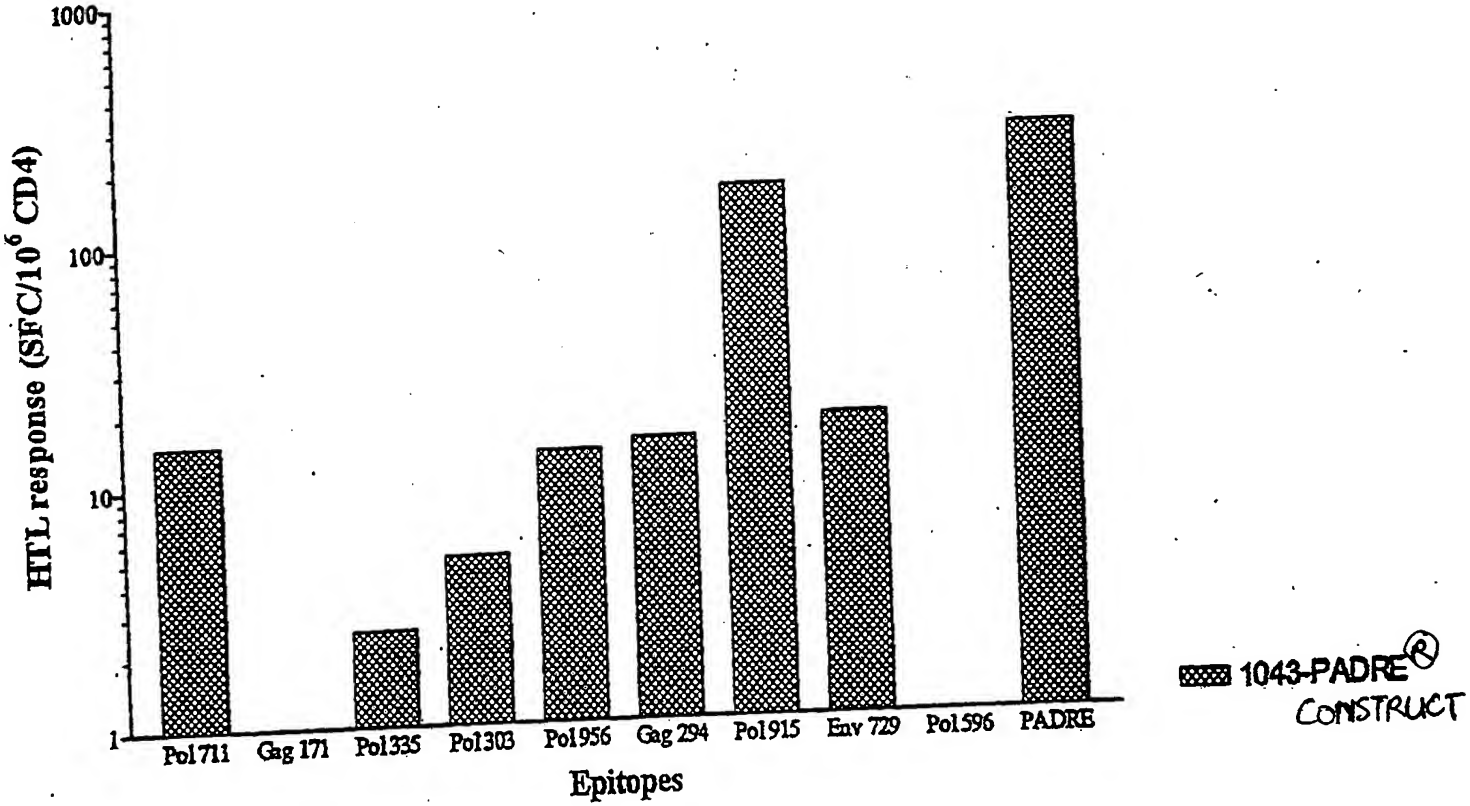
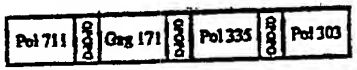
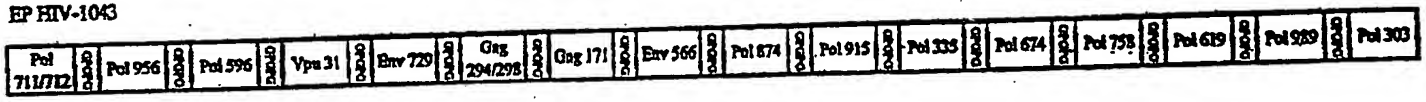

1000
100
10
1
HTL response (SFC/10^6 CD4)
Pol711
Gag 171
Pol335
Pol303
Pol956
Gag 294
Pol915
Env 729
Pol596
PADRE
Epitopes
1043-PADRE®
CONSTRUCT

FIGURE 16

HIV 75mer



EP HIV-1043



EP HIV-1043

FIGURE 17

EP-HIV-1090

MGMQVQIQSLFLLLLWVPGSRGKLVGKLNWAGAAILKEPVHGVNAACPKVSFEPIKIPIHYCAPA
KAKFVAAWTLKAAAKAFPVRPQVPLGAAKLTPLCVTLGAAAVLAEAMSQVKVYLAWVPAHKG
AAAAIFQSSMTKKTTLFCASDAKNIPYNPQSQGVVKHPVHAGPIANVTVYYGVPVWKKAAAQMA
VFIHNFKNAAAYPLASLRSLFNLTFGWCFKLNRILQQLLFINAKIQNFRVYYRKAAVTIKIGGQLKK
VPLQLPPLKAMTNNPPIPV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAAAGCTGGTGGGCAAACTCAACTGGGCCGGAGCTGCAATCCTGAAGGAGCCCGTCCACGG
GGTGAATGCCGCTTGCCCTAAAGTCAGCTTCGAACCAATTAAGATCCCCATTCATTACTGTGC
ACCTGCCAAAGCTAAGTTTGTGGCCGCTTGGACCCTCAAGGCCGCTGCAAAAGCCTTCCCAGT
GAGGCCCCAGGTGCCTCTGGGCGCCGCTAAACTCACACCACTGTGCGTCACTCTGGGAGCCGC
TGCAGTGCTGGCAGAGGCCATGTCCCAAGTGAAGGTGTATCTGGCTTGGGTGCCCGCCCACAA
GGGGGCCGCTGCAGCCATCTTTCAGTCTAGCATGACCAAGAAAACAACTCTGTTCTGTGCCTC
CGACGCTAAGAACATCCCTTATAATCCACAGTCTCAGGGCGTGGTCAAGCATCCCGTGCACGC
CGGACCTATTGCTAACGTGACCGTGTACTATGGGGTCCCAGTGTGGAAGAAAGCCGCTGCACA
GATGGCCGTGTTTATTCACAATTTCAAAAACGCCGCTGCATACCCCCTCGCCAGCCTGAGATC
CCTCTTCAACCTGACATTCGGCTGGTGCTTTAAGCTGAACCGGATCCTGCAGCAACTGCTCTTT
ATCAATGCTAAAATCCAGAACTTCCGCGTCTACTATAGGAAGGCTGCAGTGACTATCAAAATT
GGCGGACAACTGAAGAAAGTGCCTCTCCAGCTGCCCCCTCTCAAGGCAATGACCAACAATCC
CCCTATCCCAGTCTGA

HIV-CPT

MGMQVQIQSLFLLLLWVPGSRGIPIHYCAPAKAAKIQNFRVYYRKAAVTIKIGGQLKKAKFVAAW
TLKAAAKVPLQLPPLKAIFQSSMTKKLTPLCVTLGAQMAVFIHNFKGAKVYLAWVPAHKNAIPYN
PQSQGVVKAILKEPVHGVGAAALTFGWCFKLNAVLAEAMSQVNRILQQLLFINAAACPKVSFEPI
KVTVYYGVPVWKKAAHPVHAGPIANAAAYPLASLRSLFNAAATTLFCASDAKNKLVGKLNWAN
AAAFPVRPQVPLNMINNPPIPV

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAATCCCCATTCACTACTGCGCCCCTGCTAAGGCAGCCAAAATCCAGAACTTCAGGGTGTAT
TACAGAAAGGCTGCAGTCACCATTAAAATCGGCGGACAACTGAAGAAAGCCAAGTTTGTGGC
CGCTTGGACACTCAAGGCCGCTGCAAAGGTCCCACTGCAGCTCCCCCCTCTGAAGGCCATCTT
CCAGAGCTCCATGACTAAGAAACTGACCCCACTGTGTGTGACACTCGGGGCCCAGATGGCTGT
GTTCATCCATAATTTTAAAGGCGCCAAGGTCTACCTGGCTTGGGTGCCCGCACACAAGAACGC
CATTCCTTACAATCCACAGTCTCAAGGAGTGGTCAAAGCTATTCTGAAGGAGCCCGTGCACGG
GGTGGGCGCCGCTGCACTCACTTTCGGATGGTGCTTTAAACTGAACGCCGTGCTGGCTGAAGC
CATGAGCCAGGTCAATCGGATCCTGCAGCAACTGCTCTTCATTAACGCCGCTGCATGTCCTAA
GGTGTCCTTCGAGCCAATCAAAGTGACCGTGTATTACGGGGTCCCCGTGTGGAAGAAAGCCGC
TCATCCTGTCCACGCAGGCCCAATCGCCAACGCCGCTGCATATCCCCTCGCCTCTCTGCGCAG
CCTGTTTAACGCCGCTGCAACAACCCTCTTTTGCGCCTCCGACGCTAAGAATAAACTGGTGGG
AAAGCTGAACTGGGCCAACGCAGCTGCATTCCCTGTGAGGCCACAGGTCCCCCTCAATATGAC
TAACAATCCCCCTATCCCAGTGTGA

FIGURE 18A

HIV-FT
MQVQIQSLFLLLLWVPGSRGKLVGKLNWAMASDFNLFPVAIFQSSMTKVTIKIGGQLKRILQQLLF
IMAVFIHNFKIPYNPQSQGVVTTLFCASDAKILKEPVHGVQMAVFIHNFKGAAVFIHNFKRCPKVSF
EPIKIQNFRVYYRLTFGWCFKLQVPLRPMTYKMTNNPPIPVTVYYGVPVWKVLAEAMSQVIPIHY
CAPAKLTPLCVTL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAAG
CTGGTGGGGAAGCTGAACTGGGCCATGGCCAGCGATTTCAACCTGCCCCCCGTGGCCATCTTC
CAGAGCAGCATGACCAAGGTGACCATCAAGATCGGGGGGGCAGCTGAAGAGGATCCTGCAGCA
GCTGCTGTTCATCATGGCCGTGTTCATCCACAACTTCAAGATCCCCTACAACCCCCAGAGCCA
GGGGGTGGTGACCACCCTGTTCTGCGCCAGCGATGCCAAGATCCTGAAGGAGCCCGTGCACG
GGGTGCAGATGGCCGTGTTCATCCACAACTTCAAGGGCGCCGCCGTGTTCATCCACAACTTCA
AGAGGTGCCCCAAGGTGAGCTTCGAGCCCATCAAGATCCAGAACTTCAGGGTGTACTACAGG
CTGACCTTCGGGTGGTGCTTCAAGCTGCAGGTGCCCCTGAGGCCCATGACCTACAAGATGACC
AACAACCCCCCCATCCCCGTGACCGTGTACTACGGGGTGCCCGTGTGGAAGGTGCTGGCCGAG
GCCATGAGCCAGGTGATCCCCATCCACTACTGCGCCCCCGCCAAGCTGACCCCCCTGTGCGTG
ACCCTG

FIGURE 18B

HIV-TC

MGMQVQIQSLFLLLLWVPGSRGYWQATWIPEWKAIFQSSMTKKVYLAWVPAHKNAACPKVSFE
PIKHPVHAGPIANLTFGWCFKLNKMIGGIGGFIKFRDYVDRFYKAAARILQQLLFINTTLFCASDAK
NQMVHQAISPRGAKLVGKLNWAGAAAIYETYGDTWKAAQVPLRPMTYKGAAAVTVLDVGDAY
NAAARYLKDQQLLNTLNFPISPINMTNNPPIPVNAPYNTPVFAIKAAAVPLQLPPLKAAIPYNPQSQ
GVVKALLQLTVWGIGAAILKEPVHGVNAAAFPISPIETVKVWKEATTTLFKAAAVTIKIGGQLKKI
YQEPFKNLKAAAVLAEAMSQVNLVGPTPVNIGAAAEVNIVTDSQYKAAAIPIHYCAPAKAVIYQY
MDDLYKAAAQMAVFIHNFKNAATYQIYQEPFKPYNEWTLELKAKIQNFRVYYRKAFPVRPQVPL
GAAAIWGCSGKLIKVMIVWQVDRNAAKAACWWAGIKAKFVAAWTLKAAAKLTPLCVTLNAAM
ASDFNLPPVKSLLNATDIAVNVTVYYGVPVWKKAAAAIIRILQQLKRAMASDFNLNAAAYPLASL
RSLF

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCTAGA
GGATACTGGCAAGCTACTTGGATTCCAGAATGGAAAGCTATCTTTCAATCCTCAATGACGAAG
AAGGTATACCTGGCATGGGTCCCAGCACACAAGAACGCCGCTTGCCCAAAGGTGTCCTTTGAA
CCCATTAAACACCCAGTGCACGCAGGGCCAATAGCGAATTTGACATTCGGGTGGTGCTTCAAA
CTAAACAAAATGATCGGCGGCATTGGAGGCTTTATCAAGTTTAGAGATTACGTGGACCGATTC
TATAAAGCCGCTGCCCGTATACTCCAGCAGCTACTATTCATCAACACCACTCTCTTCTGCGCTT
CAGACGCTAAGAACCAAATGGTACACCAAGCCATAAGCCCTAGAGGAGCCAAGCTCGTAGGG
AAATTAAATTGGGCGGGTGCAGCAGCAATCTACGAGACTTACGGCGATACCTGGAAAGCAGC
CCAGGTTCCGTTACGCCCAATGACCTATAAAGGCGCAGCAGCAGTAACAGTTCTAGATGTAGG
AGACGCTTACAACGCTGCCGCAAGATACCTAAAAGATCAGCAGTTACTCAACACACTAAATTT
CCCAATTAGCCCGATAAACATGACAAATAACCCACCAATTCCCGTCAATGCTCCCTACAACAC
TCCAGTATTCGCAATCAAAGCCGCTGCTGTCCCCCTGCAGCTCCCTCCTCTGAAAGCTGCGAT
ACCTTACAACCCACAGAGCCAAGGTGTTGTCAAAGCACTGCTTCAGCTAACAGTTTGGGGAAT
TGGTGCTGCAATTCTAAAAGAGCCAGTTCATGGGGTTAACGCCGCCGCCTTCCCAATCAGTCC
TATTGAGACTGTGAAAGTATGGAAAGAAGCCACAACCACACTTTTTAAGGCAGCCGCAGTTA
CAATTAAAATAGGGGGCCAACTTAAGAAAATATACCAGGAACCTTTCAAGAATCTCAAAGCC
GCTGCAGTGCTCGCCGAGGCTATGTCACAGGTGAATTTGGTCGGACCAACACCCGTAAACATC
GGAGCCGCAGCCGAAGTGAACATAGTCACCGACTCACAGTACAAAGCCGCTGCAATACCCAT
ACATTATTGTGCTCCCGCAAAGGCCGTGATCTATCAATATATGGACGACCTGTATAAGGCCGC
CGCGCAGATGGCAGTCTTTATCCACAACTTTAAAAACGCAGCTACTTATCAGATCTACCAGGA
ACCATTCAAACCGTACAATGAGTGGACCTTGGAACTAAAGGCCAAAATTCAGAACTTCAGGG
TATATTATAGAAAAGCATTTCCAGTGAGGCCCCAGGTGCCTCTGGGTGCCGCAGCAATATGGG
GATGTTCTGGAAAACTGATCAAGGTGATGATTGTATGGCAAGTGGACAGAAATGCAGCTAAG
GCAGCCTGTTGGTGGGCAGGTATAAAAGCAAAGTTCGTGGCAGCATGGACGCTTAAAGCAGC
CGCAAAACTCACTCCTCTCTGCGTGACACTTAATGCAGCCATGGCCTCTGATTTCAACCTTCCC
CCTGTAAAATCCCTGCTTAATGCGACAGATATCGCAGTCAACGTAACAGTATATTATGGCGTG
CCAGTCTGGAAAAAAGCCGCCGCGGCCATAATTCGGATACTGCAGCAGCTGAAAAGAGCTAT
GGCGAGTGACTTCAACCTGAATGCGGCCGCCTACCCCTTGGCATCGTTAAGGTCACTATTTTG
A

FIGURE 18C

HCV.1
MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVDLMGYIPLVYLVAYQATVILAGYGAGVRLIVFP
DLGVHMWNFISGIYLLPRRGPRLYLVTRHADVVLVGGVLAALLFLLLADAFLLLADARVVWMNRL
IAFACTCGSSDLYLSAFSLHSYGVAGALVAFKLPGCSFSIFKTSERSQPRLIFCHSKKKFWAKHMW
NFIPFYGKAIRMYVGGVEHRQLFTFSPRRRLGVRATRKVGIYLLPNRAKFVAAWTLKAAA*

GAATTCGCCGCCACCATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCC
GGATCCAGAGGACTGCTGTTCAACATCCTGGGGGGGTGGGTGGATCTGATGGGGTACATCCCC
CTGGTGTACCTGGTGGCCTACCAGGCCACCGTGATCCTGGCCGGGTACGGGGCCGGGGTGAG
GCTGATCGTGTTCCCCGATCTGGGGGTGCACATGTGGAACTTCATCAGCGGGATCTACCTGCT
GCCCAGGAGAGGACCTAGACTGTACCTGGTGACTAGACACGCTGATGTGGTGCTGGTGGGAG
GAGTGCTGGCTGCTCTGCTGTTTCTGCTGCTGGCTGATGCTTTCCTGCTGCTGGCTGATGCTAG
AGTGTGGATGAACAGACTGATCGCTTTCGCTTGTACATGTGGAAGCTCCGATCTGTATCTGAG
CGCTTTCAGCCTGCACAGCTACGGAGTGGCTGGAGCTCTGGTGGCTTTTAAGCTGCCTGGATG
TAGCTTTAGCATCTTTAAGACCAGCGAAAGAAGCCAGCCTAGACTGATCTTTTGTCACAGCAA
GAAGAAGTTTTGGGCTAAGCACATGTGGAATTTTATCCCTTTCTATGGAAAGGCTATCAGAAT
GTATGTGGGAGGAGTGGAACACAGACAGCTGTTTACATTTAGCCCTAGAAGGAGACTGGGAG
TGAGAGCTACAAGAAAGGTGGGAATCTATCTGCTGCCTAATAGATGAAAGCTTGGG*

HCV.2
MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAALLFLLLADALIFCHSKKKQLF
TFSPRRYLVTRHADVYLLPRRGPRLCTCQSSDLYHMWNFISGIFWAKHMWNFAKFVAAWTLKAA
AILAGYGAGVYLVAYQATVGVAGALVAFKIPFYGKAIRMYVGGVEHRVLVGGVLAAFLLLADA
RVLPGCSFSIFAKFVAAWTLKAAAKTSERSQPRRLGVRATRKRLIVFPDLGVWMNRLIAFALSAFS
LHSYLLFNILGGWVVGIYLLPNR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGATCTGATGGGATATATCCCTCTGGTGGCTAAGTTTGTGGCTGCT
TGGACACTGAAGGCTGCTGCTCTGCTGTTTCTGCTGCTGGCTGATGCTCTGATCTTCTGTCACA
GCAAGAAGAAGCAGCTGTTTACATTTAGCCCAAGAAGATATCTGGTGACAAGACACGCTGAT
GTGTATCTGCTGCCTAGACGCGGACCTAGACTGTGTACATGTGGAAGCTCCGATCTGTATCAC
ATGTGGAACTTTATCAGCGGAATCTTTTGGGCTAAGCACATGTGGAATTTCATCCTGGCTGGA
TATGGAGCTGGAGTGTATCTGGTGGCTTATCAGGCTACAGTGGGAGTGGCTGGAGCTCTGGTG
GCTTTCAAGATCCCATTCTATGGAAAGGCTATCAGAATGTATGTGGGAGGAGTGGAACACAG
AGTGCTGGTGGGAGGAGTGCTGGCTGCTTTCCTGCTGCTGGCTGATGCTAGAGTGCTGCCAGG
ATGTAGCTTTAGCATCTTCAAGACTTCCGAACGCTCCCAGCCTAGAAGACTGGGAGTGAGAGC
TACAAGGAAGAGACTGATCGTGTTTCCAGATCTGGGAGTGTGGATGAATAGACTGATCGCTTT
CGCTCTGAGCGCTTTCAGCCTGCACAGCTATCTGCTGTTCAACATCCTGGGAGGATGGGTGGT
GGGAATCTATCTGCTGCCAAACAGATGAAAGCTT

HCV.3s1
MGMQVQIQSLFLLLLWVPGSRGYLVAYQATVAKFVAAWTLKAAALLFLLLADALIFCHSKKKYL
VTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNF*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGATACCTCGTCGCCTACCAGGCCACTGTGGCTAAATTCGTGGCAGCC
TGGACACTGAAAGCTGCAGCTCTGCTCTTCCTGCTCCTGGCCGATGCACTCATCTTCTGCCATT
CCAAGAAAAAGTATCTGGTCACCAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAGC
AAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGTGGAACTTTATTTCTGGAATCTTTTGGG
CCAAGCACATGTGGAATTTCTGAAAGCTT

FIGURE 18D

HCV.3s2
MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLLADARVLSAFSLHSYIL
AGYGAGVWMNRLIAFAIPFYGKAIVAGALVAFKVGIYLLPNR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTCGCTGCT
TGGACACTGAAGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGC
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT
GCCATTCCATTCTATGGGAAAGCCATTGTGGCTGGCGCCCTGGTGGCATTCAAGGTCGGGATC
TACCTCCTGCCTAACCGCTGAAAGCTT

HCV.3s2(-3)
MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLLADARVLSAFSLHSYIL
AGYGAGVWMNRLIAFA*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTCGCTGCT
TGGACACTGAAGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGC
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT
GCCTGAGGATCC

HCV.3s3
MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAARLGVRATRKLLFNILGGWV
RMYVGGVEHRRLIVFPDLGVGVAGALVAFKLPGCSFSIFKTSERSQPRQLFTFSPRRYLLPRRGPRL

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAGACCTGATGGGCTACATCCCTCTCGTGGCCAAGTTTGTGGCAGCT
TGGACCCTGAAGGCCGCTGCCAGACTGGGAGTGCGCGCTACACGGAAACTCCTGTTTAACATC
CTGGGAGGGTGGGTGCGGATGTACGTCGGAGGCGTCGAGCACAGAAGGCTCATTGTCTTTCC
AGATCTCGGCGTGGGCGTCGCAGGCGCACTCGTGGCCTTCAAACTGCCAGGGTGCAGCTTCAG
CATTTTCAAGACCTCCGAACGCTCCCAACCCAGACAGCTGTTCACTTTCTCTCCTCGGAGGTAT
CTGCTGCCCAGACGCGGACCCAGGCTGTGAAAGCTT

HCV.PC3
MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVKAKFVAAWTLKAAALADGGCSGGAYRLIVFPD
LGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPRR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGACTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCCAAGTTCGTG
GCTGCCTGGACCCTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCGGAGCTTACAG
GCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGAATTTCATCGG
GGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCCAAGACGGTGAGG
TACC

FIGURE 18E

HGV.PC4
MGMQVQIQSLFLLLLWVFGSRGRLGVRATRKKAKFVAAWTLKAAAKTSERSQPRNLPGCSFSIFN
DLMGYIPLVKYLLPRRGPRLNTLCGFADLMGYRMYVGGVEHR*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGATCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCCAAGTTCGTGGC
TGCCTGGACCCTGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTG
GATGCTCTTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCC
CAGACGGGGCCCTCGCCTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTA
TGTCGGCGGAGTCGAACACAGATGAGGTACC

HCV.2431(1P)
MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAFLLLADARVLSAFSLHSYILAGYGAGVWMNRL
IAFAGAAARLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVKYLLPRRGPRLNTLCG
FADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFPDLGVKFWAKHMWN
FIGVAGALVAFKKQLFTFSPRRNGYLVAYQATVAAALLFLLLADALIFCHSKKKYLVTRHADVLG
FGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKAAAAKFVAAWTLKAAA

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGCTCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCAGCCGCTTTCCTGCTCCTGGCA
GACGCCAGGGTGCTGTCTGCCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGC
GTGTGGATGAATCGGCTGATCGCCTTTGCCGGCGCTGCCGCAAGGCTGGGCGTGAGAGCCACC
CGGAAGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTC
TTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGG
GGCCCTCGCCTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTATGTCGGC
GGAGTCGAACACAGAAAACTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCT
GGCCGACGGGGGATGCAGCGGCGGAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAA
ATTTTGGGCAAAGCACATGTGGAATTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAA
GCAGCTCTTCACCTTCTCCCCAAGACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGC
TGCAGCTCTGCTCTTCCTGCTCCTGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTAT
CTGGTCACCAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAGCAAGTGCACCTGTGGC
AGCTCCGACCTGTATCACATGTGGAACTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGG
AATTTTAAGGCCGCAGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAGG
ATCC

FIGURE 18F

HCV.4312(1P)
MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVK
YLLPRRGPRLNTLCGFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFP
DLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPRRNGYLVAYQATVAAALLFLLLADALIFCHS
KKKYLVTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKKAAAVLVGGVLAA
AFLLLADARVLSAFSLHSYILAGYGAGVWMNRLIAFANAAAKFVAAWTLKAAA*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG
GTGCCCGGCTCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAAAC
AAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTCTTTCAGCATCTTTAATGACCTCAT
GGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGGGGCCCTCGCCTGAACACTCTCTG
TGGATTTGCTGATCTGATGGGGTACAGGATGTATGTCGGCGGAGTCGAACACAGAAAACTGCT
CTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCG
GAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGA
ATTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCCAA
GACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGCTGCAGCTCTGCTCTTCCTGCTCC
TGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACG
TGCTGGGGTTTGGCGCCTACATGAGCAAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGT
GGAACTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGGAATTTTAAGAAAGCCGCTGCAG
TCCTGGTGGGCGGCGTCCTGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGCTGTCTG
CCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGA
TCGCCTTTGCCAATGCTGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAG
GATCC

AOSI.K
MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVKFLLSLGIH
LYMDDVVLGVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKWLSLLVPFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGAAGTTCCTGGTGTCCCTGGGAA
TCCACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGT
TCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG
CCTTCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGTGA

HBV.1
MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVFLLSLGIHL
YMDDVVLGVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKWLSLLVPFVIPIPSSWAFTP
ARVTGGVFKVGNFTGLYLPSDFFPSVTLWKAGILYKNVSIPWTHKLVVDFSQFSRSAICSVVRRAL
MPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGTTCCTGCTGTCCCTGGGAATCC
ACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCC
TGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGGCCT
TCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGATCCCTATCCCTAG
CTCCTGGGCTTTCACCCCAGCCAGGGTGACCGGAGGAGTGTTTAAGGTGGGAAACTTCACCGG
CCTGTATCTGCCCAGCGATTTCTTTCCTAGCGTGACCCTGTGGAAGGCCGGGATCCTGTACAA
GAATGTGTCCATCCCTTGGACCCACAAGCTGGTGGTGGACTTTTCCCAGTTCAGCAGATCCGC
TATCTGCTCCGTGGTGAGGAGAGCTCTGATGCCACTGTATGCCTGTATCTGA

FIGURE 18G

HBV.2
MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVNFLLSLGIH
LYMDDVVLGVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWLSLLVPFVNIPIP
SSWAFKTPARVTGGVFKVGNFTGLYNLPSDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVDFSQ
FSRNSAICSVVRRALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGGTCCAGA
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGAACTTCCTGCTGTCCCTGGGAA
TCCACCTGTATATGGATGACGTGGTGCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGT
TCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG
CCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCTGCTGGTGCCCTTTGT
GAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGACCGGAGGAGTGTT
TAAGGTGGGAAACTTCACCGGCCTGTATAACCTGCCCAGCGATTTCTTTCCTAGCGTGAAGAC
CCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCG
CTCTGGTGGTGGACTTTCCCAGTTCAGCAGAAATTCCGCTATCTGCTCCGTGGTGAGGAGAG
CTCTGATGCCACTGTATGCCTGTATCTGA

PfCTL.1
MQVQIQSLFLLLLWVPGSRGILSVSSFLFVNAAAQTNFKSLLRNLPSENERGYKAAALLACAGLAY
KKAAAAKFVAAWTLKAAAKAFMKAVCVEVNAAASFLFVEALFNATPYAGEPAPFKAAAKYKLA
TSVLKAGVSENIFLKNAAAYFILVNLLIKAGLLGVVSTV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA
GGAATCCTGAGCGTGTCCTCTTTCCTGTTTGTCAACGCCGCTGCACAGACCAATTTCAAGAGC
CTCCTGAGGAACCTCCCCTCCGAGAACGAAAGAGGCTACAAAGCCGCTGCACTGCTCGCCTGC
GCTGGACTGGCCTATAAGAAAGCCGCTGCAGCCAAGTTCGTGGCCGCTTGGACACTGAAGGC
CGCTGCAAAAGCCTTTATGAAGGCTGTCTGTGTGGAGGTCAATGCCGCTGCATCTTTCCTGTTT
GTGGAGGCCCTCTTTAACGCTACTCCTTACGCAGGGGAACCAGCCCCCTTCAAGGCCGCTGCA
AAATATAAGCTGGCAACCAGCGTGCTGAAGGCTGGCGTGTCCGAGAATATTTTTCTGAAAAAC
GCCGCTGCATACTTCATCCTGGTGAATCTGCTCATTAAGGCCGGACTCCTGGGGGGTGGTCTCT
ACAGTGTGA

PfCTL.2
MQVQIQSLFLLLLWVPGSRGFVEALFQEYNAAAKYLVIVFLINALACAGLAYKKFYFILVNLLKA
ALFFIIFNKNAAAKFVAAWTLKAAAKFILVNLLIFHNFQDEENIGIYKLPYGRTNLKAAAVLLGGV
GLVLNFLIFFDLFLVKAVLAGLLGVV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA
GGATTCGTGGAGGCCCTGTTTCAGGAATACAACGCCGCTGCAAAGTATCTCGTCATCGTGTTC
CTGATCAATGCTCTGGCATGCGCCGGCCTCGCTTACAAAAAGTTTTACTTCATTCTGGTCAACC
TGCTCAAGGCCGCTCTGTTCTTTATCATTTTCAATAAAAACGCCGCAGCTAAGTTTGTGGCCGC
ATGGACCCTGAAGGCCGCTGCAAAATTCATCCTCGTGAATCTGCTCATTTTTCACAACTTCCAA
GACGAGGAAAATATCGGAATTTATAAGCTGCCCTACGGGAGGACAAACCTGAAAGCCGCTGC
AGTCCTGCTCGGCGGAGTGGGGCTGGTGCTCAATTTTCTGATCTTCTTTGATCTGTTCCTGGTG
AAGGCCGTCCTGGCCGGCCTGCTCGGAGTCGTGTGA

FIGURE 18H

PACTL3
MQVQIQSLFLLLLWVPGSRGVFLIFFDLFLNAAAPSDGKCNLYKAAAVTCGNGIQVRKLFHIFDGD
NEIKAHVLSHNSYEKNYYGKQENWYSLKKILSVFFLANAAAKFIKSLFHIFKAAALYISFYFIKAKF
VAAWTLKAAAKAAAYYIPHQSSLKAAAGLIMVLSFL

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA
GGAGTGTTCCTGATCTTCTTTGACCTGTTCCTGAACGCCGCTGCACCCAGCGATGGCAAGTGC
AATCTCTACAAGGCCGCTGCAGTGACCTGTGGAAACGGGATTCAGGTCAGGAAACTCTTTCAC
ATCTTCGACGGCGATAACGAGATCAAGGCCCATGTGCTGTCCCACAATTCTTATGAAAAAAAC
TACTATGGAAAGCAAGAGAATTGGTACAGCCTGAAGAAAATTCTGTCCGTGTTCTTTCTGGCC
AACGCCGCTGCAAAGTTTATCAAGTCTCTGTTCCATATTTTCAAGGCCGCTGCACTCTACATCA
GCTTCTATTTTATTAAAGCCAAATTTGTGGCCGCTTGGACACTGAAGGCCGCTGCAAAAGCCG
CTGCATACTATATCCCTCACCAGAGCTCCCTGAAGGCCGCTGCAGGGCTGATCATGGTGCTCT
CTTTCCTGTGA

PACTL/HTL(N)
MQVQIQSLFLLLLWVPGSRGSSVFNVVNSSIGLIMVLSFLGPGPGLYISFYFILVNLLIFHINGKIIKN
SEGPGPGPDSIQDSLKESRKLSGPGPGVLAGLLGVVSTVLLGGVGLVLGPGPGLPSENERGYYIPHQ
SSLGPGPGQTNFKSLLRNLGVSENIFLKGPGPGFQDEENIGIYGPGPGKYLVIVFLIFFDLFLVGPGP
GKFIKSLFHIFDGDNEIGPGPGKSKYKLATSVLAGLLGPGPGLPYGKTNLGPGPGRHNWVNHAVPL
AMKLIGPGPGMRKLAILSVSSFLFVEALFQEYGPGPGVTCGNGIQVRGPGPGMNYYGKQENWYSL
KKGPGPGPSDGKCNLYADSAWENVKNVIGPFMKAVCVEVGPGPGKILSVFFLALFFIIFNKGPGPG
HVLSHNSYEKGPGPGKYKIAGGIAGGLALLACAGLAYKFVVPGAATPYAGEPAPF

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA
GGAAGTAGTGTGTTCAATGTTGTGAACTCATCAATTGGTCTGATCATGGTGCTGAGCTTTCTCG
GGCCAGGGCCAGGATTATATATTTCTTTCTACTTCATCCTTGTCAACCTGTTAATATTCCACAT
TAACGGCAAAATAATAAAGAACAGTGAAGGCCCTGGGCCTGGGCCTGACTCGATCCAGGATT
CTCTAAAAGAATCGAGGAAGCTCTCCGGACCAGGCCCTGGTGTACTCGCCGGGTTGCTGGGA
GTAGTTAGCACAGTGCTGTTAGGAGGCGTCGGCCTCGTCTTAGGACCTGGACCAGGTCTGCCG
TCCGAAAACGAAAGAGGATACTACATACCTCACCAGAGCAGCCTCGGCCCAGGCCCCGGACA
AACCAATTTCAAATCCCTCTTGCGAAATCTAGGAGTGAGCGAGAACATATTTCTTAAAGGACC
CGGTCCCGGCTTTCAGGACGAGGAGAATATAGGTATTTACGGTCCAGGACCTGGAAAATACCT
AGTGATCGTATTCCTAATTTTTTTTGACCTATTTCTGGTGGGCCCAGGTCCCGGAAAGTTCATT
AAATCACTCTTCCACATTTTTGACGGAGATAACGAGATAGGACCCGGTCCCGGGAAATCAAA
GTACAAACTAGCCACTTCAGTGCTGGCCGGCCTTCTAGGGCCGGGCCCAGGGCTCCCCTATGG
AAAGACAAATCTTGGCCCCCGGTCCAGGACGGCACAACTGGGTGAATCATGCGGTTCCATTGG
CCATGAAACTAATCGGGCCCGGTCCAGGCATGCGCAAACTTGCAATTCTAAGCGTAAGTTCAT
TTCTGTTCGTAGAGGCACTGTTTCAAGAATATGGCCCAGGACCTGGCGTCACATGTGGGAATG
GGATCCAGGTGAGAGGACCGGGACCTGGTATGAACTATTACGGTAAACAGGAAAATTGGTAC
TCCCTGAAAAAGGGTCCAGGCCCCGGCCCCTCAGATGGTAAGTGCAACCTGTATGCTGACTCA
GCATGGGAGAACGTAAAAAATGTAATAGGCCCATTCATGAAGGCAGTTTGTGTCGAAGTCGG
ACCAGGCCCAGGAAAAATACTTTCTGTCTTCTTCCTAGCTCTCTTCTTCATCATCTTCAACAAG
GGACCAGGGCCAGGTCACGTGTTATCCCATAACTCTTATGAAAAAGGGCCAGGACCTGGGAA
ATACAAAATCGCAGGAGGGATCGCCGGCGGGCTAGCGCTCCTTGCCTGCGCAGGCTTGGCTTA
CAAATTCGTTGTACCAGGAGCTGCAACACCCTATGCAGGAGAACCTGCCCCATTTTGAAGATC
TGC

FIGURE 18I

PB3
MGMQVQIQSLFLLLLWVPGSRGFMKAVCVEVNVTCGNGIQVRKGLIMVLSFLNAALFHIFDGDN
EIKAALLACAGLAYKKSFLFVEALFNAAPSDGKCNLYKAAQTNFKSLLRNLPSENERGYKAAGVS
ENIFLKNAAAYFILVNLLIKAAAILSVSSFLFVNTPYAGEPAPFKAAAKYKLATSVLKAAVFLIFFDL
FLNYYIPHQSSLKAAGLLGNVSTVGAVLLGGVGLVLNLACAGLAYKKAKFIKSLFHIFKAAFYFIL
VNLLKAFLIFFDLFLVKALFFIIFNKNYYGKQENWYSLKFVEALFQEYNAAAKFVAAWTLKAAAK
ILSVFFLANAVLAGLLGNVNFQDEENIGIYKAAALYISFYFIKAFILVNLLIFHNAALPYGRTNLKAA
HVLSHNSYEKNAAAKYLVIVFLI

GCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCC
GGATCCAGAGGATTTATGAAAGCTGTCTGTGTAGAGGTGAATGTAACATGCGGTAACGGAAT
TCAGGTGAGAAAGGGACTCATCATGGTACTCAGCTTTCTGAACGCAGCCCTGTTCCACATCTT
TGACGGAGACAATGAAATCAAAGCCGCATTGCTCGCCTGTGCCGGACTAGCCTATAAAAAGA
GTTTCCTTTTCGTTGAAGCACTATTTAACGCAGCACCCAGTGACGGTAAATGCAACCTATATA
AAGCAGCTCAGACTAATTTCAAAAGCCTGTTAAGAAATCTGCCCTCAGAGAATGAAAGGGGT
TACAAAGCCGCCGGCGTGTCCGAGAATATTTTCCTGAAGAACGCCGCTGCTTATTTTATACTC
GTGAATCTACTCATAAAGGCAGCCGCAATCCTTTCAGTGTCCAGCTTTCTGTTTGTTAACACAC
CATATGCGGGCGAGCCGGCTCCTTTCAAGGCTGCAGCAAAATACAAGCTTGCCACATCAGTAT
TGAAAGCAGCTGTGTTTTTGATATTCTTTGATCTTTTTTTAAACTACTACATACCTCATCAGTCT
AGTCTTAAAGCAGCCGGGCTACTGGGGAACGTCTCTACTGTGGGGGCCGTCTTACTTGGAGGA
GTTGGCCTCGTGTTGAACCTCGCGTGCGCAGGTCTGGCCTACAAAAAAGCGAAATTCATCAAG
TCTCTGTTCCACATTTTTAAAGCCGCATTCTATTTCATACTAGTGAACCTTCTCAAAGCTTTCCT
GATCTTCTTCGATCTATTCCTCGTAAAAGCGCTATTCTTCATTATCTTTAACAAAAATTATTAC
GGCAAGCAAGAAAATTGGTACTCACTCAAGTTTGTAGAAGCTCTGTTCCAGGAATACAACGCC
GCTGCTAAATTCGTTGCAGCTTGGACCCTGAAAGCAGCTGCAAAGATCCTATCGGTCTTCTTTC
TCGCTAATGCCGTATTAGCAGGACTTCTAGGCAACGTGAACTTTCAAGACGAAGAGAATATAG
GCATCTACAAAGCCGCAGCACTGTACATTTCATTCTACTTCATCAAGGCCTTCATACTGGTCAA
CCTTCTGATATTTCATAATGCAGCACTGCCATATGGGAGAACCAACTTGAAAGCGGCCCACGT
GTTGAGCCACAACTCCTACGAGAAGAACGCCGCCGCGAAATATCTCGTCATTGTCTTCCTGAT
TTGA

TB.1
MQVQIQSLFLLLLWVPGSRGRMSRVTTFTVKALVLLMLPVVNLMIGTAAAVVKALVLLMLPVGA
GLMTAVYLVGAAAMALLRLPVKRMFAANLGVNSLYFGGICVGRLPLVLPAVNAAAAKFVAAWT
LKAAAKAAARLMIGTAAAGFVVALIPLVNAMTYAAPLFVGAAAAMALLRLPLV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGAAGG
ATGAGCAGAGTGACCACATTCACTGTCAAGGCCCTGGTGCTCCTGATGCTCCCCGTCGTGAAC
CTGATGATCGGCACCGCTGCAGCCGTCGTGAAAGCTCTCGTCCTGCTCATGCTCCCTGTGGGA
GCAGGGCTGATGACAGCCGTGTACCTGGTCGGCGCTGCAGCCATGGCCCTCCTGCGGCTGCCA
GTGAAGCGCATGTTTGCTGCAAATCTGGGAGTCAACTCCCTCTATTTCGGGGGCATTTGCGTG
GGAAGGCTGCCCCTCGTGCTGCCTGCTGTGAATGCAGCCGCTGCCAAATTTGTCGCCGCTTGG
ACTCTGAAGGCAGCCGCTAAGGCCGCTGCAAGACTGATGATCGGGACCGCCGCTGCCGGCTT
CGTGGTCGCCCTGATTCCCCTGGTGAACGCCATGACATACGCAGCTCCTCTGTTTGTGGGAGC
CGCTGCAGCCATGGCTCTCCTGCGGCTGCCACTGGTGTGA

FIGURE 18J

BCL A2 #90
MQVQIQSLFLLLLWVPGSRGIMIGHLVGVNRLLQETELVNAKVAEIVHFLNAKVFGSLAFVNAYL
SGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAAAVVLGVVFGINSMPPPGTRVNAAA
ATVGIMIGVNAKLCPVQLWV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGGTCCAGAGGAATT
ATGATCGGCCATCTGGTGGGCGTCAACAGACTGCTGCAGGAAACCGAGCTGGTGAATGCCAA
GGTGGCCGAAATTGTGCACTTTCTCAACGCAAAGGTGTTTGGTTCCCTGGCTTTTGTCAATGCC
TATCTGAGCGGCGCTAACCTCAACGTCGGAGCCGCCTACCTCCAGCTGGTCTTCGGCATCGAG
GTCAACGCTGCTGCAAAATTCGTGGCAGCTTGGACCCTCAAGGCTGCAGCAAAGGCTGCCGCC
GTCGTGCTCGGAGTGGTGTTCGGGATCAACTCTATGCCACCTCCCGGGACTAGGGTCAATGCT
GCCGCCGCAACAGTGGGAATCATGATTGGGGTGAATGCCAAACTGTGCCCAGTGCAACTGTG
GGTGTGA

BCL A2 #88
MQVQIQSLFLLLLWVPGSRGVVLGVVFGINAAAAKFVAAWTLKAAAKVAEIVHFLNAYLSGANL
NVGAAYLQLVFGIEVNIMIGHLVGVNRLLQETELVNAKVFGSLAFVNAKLCPVQLWVNAAAATV
GIMIGVNSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGGTCCAGAGGAGTC
GTGCTGGGAGTCGTCTTCGGCATTAATGCCGCCGCTGCAAAGTTCGTGGCTGCCTGGACCCTG
AAGGCCGCAGCTAAAGTGGCAGAGATCGTGCACTTTCTGAACGCCTACCTGAGCGGAGCAAA
TCTGAACGTCGGCGCTGCCTATCTGCAGCTCGTGTTTGGAATTGAAGTGAACATCATGATTGG
ACATCTGGTGGGCGTGAACAGGCTGCTCCAGGAAACTGAGCTGGTCAACGCTAAAGTGTTCG
GGTCTCTCGCCTTTGTGAACGCTAAGCTCTGCCCCGTCCAACTCTGGGTCAATGCCGCAGCCG
CTACAGTGGGGATCATGATCGGCGTGAACTCCATGCCTCCACCAGGGACCAGAGTGTGA

BCL A2 #63
MQVQIQSLFLLLLWVPGSRGKLCPVQLWVNAAAATVGIMIGVNIMIGHLVGVNRLLQETELVNA
KVAEIVHFLNAKVFGSLAFVNAYLSGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAA
AVVLGVVFGINSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAAAG
CTCTGCCCCGTGCAACTGTGGGTCAACGCCGCCGCCGCAACCGTCGGCATTATGATCGGGGTG
AACATCATGATCGGACACCTGGTCGGCGTGAACAGGCTGCTGCAGGAGACAGAACTGGTCAA
TGCCAAGGTGGCTGAAATTGTCCATTTCCTGAATGCCAAAGTGTTCGGCTCTCTCGCTTTCGTG
AACGCTTATCTGAGCGGAGCTAACCTCAACGTGGGGGCCGCATACCTCCAGCTCGTCTTTGGG
ATTGAGGTGAATGCCGCAGCTAAATTTGTCGCTGCCTGGACCCTGAAGGCAGCAGCCAAGGCT
GCCGCAGTGGTGCTGGGAGTGGTGTTTGGAATCAATTCCATGCCTCCACCAGGCACTAGAGTG
TGAGGATCC

FIGURE 18K

Prostate 1
LTFFWLDRSVKAAAVLVHPQWVLTVKAAALLQERGVAYIKAALLLSIALSVNPLVCNGVLQGVK
AAIMYSAHDTTVKAAAFLTPKKLQCVNAMMNDQLMFLNAGLPSIPVHPVKAAALGTTCYVGAAI
LLWQPIPVNFLRPRSLQCVKAFLTLSVTWIGVNALLYSLVHNLGAATLMSAMTNL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATTG
ACATTTTTTTGGCTGGATAGATCGGTTAAGGCTGCAGCCGTGCTTGTTCATCCCCAGTGGGTCT
TGACCGTAAAGGCTGCCGCGCTGCTACAAGAAAGAGGGGTCGCATACATCAAAGCTGCTCTC
CTCTTGAGTATTGCGCTAAGTGTAAACCCGCTAGTTTGTAATGGGGTGTTACAAGGTGTGAAA
GCGGCGATTATGTACAGTGCCCACGACACTACCGTAAAAGCAGCCGCTTTCCTGACCCCAAAA
AAACTCCAATGCGTGAACGCAATGATGAATGATCAGCTGATGTTTTTAAACGCTGGCTTACCT
TCTATACCGGTTCATCCAGTCAAGGCCGCGGCATTGGGTACGACGTGTTATGTTGGAGCAGCG
ATACTTCTTTGGCAGCCCATACCAGTAAATTTTTTAAGACCTAGATCCTTACAATGCGTCAAAG
CATTCCTTACACTCTCAGTAACTTGGATCGGAGTCAATGCTCTGCTATATAGCCTCGTACACAA
CTTGGGCGCGGCCACACTTATGAGTGCAATGACGAATTTAGCTAAGTTCGTGGCGGCCTGGAC
TCTAAAGGCCGCAGCA

HIV-1043
MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGPGPGWEFVNTPPLVKLWYQGPGPGYR
KILRQRKIDRLIDGPGPGQHLLQLTVWGIKQLQGPGPGGEIYKRWIILGLNKIVRMYGPGPGQGQM
VHQAISPRTLNGPGPGIKQFINMWQEVGKAMYGPGPGWAGIKQEFGIPYNPQGPGPGKTAVQMA
VFIHNFKRGPGPGSPAIFQSSMTKILEPGPGPGEVNIVTDSQYALGIIGPGPGHSNWRAMASDFNLPP
GPGPGAETFYVDGAANRETKGPGPGGAVVIQDNSDIKVVPGPGPGFRKYTAFTIPSINNE

ATGGAGAAGGTGTACCTGGCCTGGGTTCCAGCCCACAAAGGCATCGGGGGAGGGCCCGGACC
TGGGCAGAAACAGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAG
GTTGGGAGTTTGTGAACACACCACCCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCGGAT
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCGGGCCCAGGCCAG
CACCTTCTGCAGCTTACAGTGTGGGGAATTAAACAGCTGCAGGGGCCGGGCCCCGGGGGGGA
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGGCCCTGGACC
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGCCCAG
GAATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTG
GATGGGCAGGGATAAAACAGGAGTTTGGAATCCCTTACAATCCCCAGGGTCCTGGGCCAGGT
AAAACGGCAGTGCAGATGGCCGTGTTCATTCATAATTTTAAGCGGGGCCCTGGACCTGGCAGC
CCAGCTATATTTCAAAGTTCGATGACCAAAATCTTGGAGCCCGGCCCAGGGCCGGGCGAAGT
GAACATTGTCACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCGGACCAGGGCATTCCAA
TTGGCGCGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGCGGAAACTTT
CTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCA
TTCAGGACAACTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCCGGGTTCAGAAAGTATACCG
CCTTCACTATTCCGTCCATCAACAATGAGTGA

FIGURE 18L

HIV-1043 PADRE
MEKVYLAWVPAHKGIGGPGPGQKQITKIQNFRVYYRGPGPGWEFVNTPPLVKLWYQGPGPGYR
KILRQRKIDRLIDGPGPGQHLLQLTVWGIKQLQGPGPGGEIYKRWIILGLNKIVRMYGPGPGQGQM
VHQAISPRTLNGPGPGIKQFINMWQEVGKAMYGPGPGWAGIKQEFGIPYNPQGPGPGKTAVQMA
VFIHNFKRGPGPGSPAIFQSSMTKILEPGPGPGEVNIVTDSQYALGIIGPGPGHSNWRAMASDFNLPP
GPGPGAETFYVDGAANRETKGPGPGGAVVIQDNSDIKVVPGPGPGFRKYTAFTIPSINNEGPGPGA
KFVAAWTLKAAA

ATGGAGAAGGTGTACCTGGCCTGGGTTCCAGCCCACAAAGGCATCGGGGGAGGGCCCGGACC
TGGGCAGAAACAGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAG
GTTGGGAGTTTGTGAACACACCACCCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCGGAT
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCGGGCCCAGGCCAG
CACCTTCTGCAGCTTACAGTGTGGGGAATTAAACAGCTGCAGGGGCCGGGCCCCGGGGGGGA
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGGCCCTGGACC
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGCCCAG
GAATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTG
GATGGGCAGGGATAAAACAGGAGTTTGGAATCCCTTACAATCCCCAGGGTCCTGGGCCAGGT
AAAACGGCAGTGCAGATGGCCGTGTTCATTCATAATTTTAAGCGGGGCCCTGGACCTGGCAGC
CCAGCTATATTTCAAAGTTCGATGACGAAAATCTTGGAGCCCGGCCCAGGGCCGGGCGAAGT
GAACATTGTCACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCGGACCAGGGCATTCCAA
TTGGCGCGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGCGGAAACTTT
CTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCA
TTCAGGACAACTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCCGGGTTCAGAAAGTATACCG
CCTTCACTATTCCGTCCATCAACAATGAGGGCCCCGGCCCAGGTGCCAAGTTCGTGGCTGCCT
GGACCCTGAAGGCTGCCGCTTGA

HIV 75mer
EKVYLAWVPAHKGIGGPGPGQGQMVHQAISPRTLNGPGPGSPAIFQSSMTKILEPGPGPGFRKYTA
FTIPSINNE

GAGAAGGTGTACCTGGCCTGGGTGCCTGCCCACAAGGGAATCGGAGGACCTGGCCCTGGACA
GGGACAGATGGTGCACCAGGCCATCAGCCCTAGGACCCTGAACGGACCTGGACCTGGAAGCC
CTGCCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCGGACCTGGACCTGGATTCAGGA
AGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGTGA

FIGURE 18M

PfHTL
MQVQIQSLFLLLLWVPGSRGRHNWVNHAVPLAMKLIGPGPGKCNLYADSAWENVKNGPGPGKS
KYKLATSVLAGLLGPGPGQTNFKSLLRNLGVSEGPGPGSSVFNVVNSSIGLIMGPGPGVKNVIGPF
MKAVCVEGPGPGMNYYGKQENWYSLKKGPGPGGLAYKFVVPGAATPYGPGPGPDSIQDSLKESR
KLNGPGPGLLIFHINGKIIKNSEGPGPGAGLLGNVSTVLLGGVGPGPGKYKIAGGIAGGLALLGPGP
GMRKLAILSVSSFLFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA
GGAAGGCACAACTGGGTGAATCATGCTGTGCCCCTGGCTATGAAGCTGATCGGCCCTGGACC
AGGGAAATGCAACCTCTACGCAGACAGCGCCTGGGAGAACGTCAAGAATGGCCCCGGACCTG
GGAAATCCAAGTATAAGCTCGCTACCTCTGTGCTGGCAGGCGTGCTCGGACCAGGCCCCGGAC
AGACAAATTTCAAAAGCCTGCTCAGAAACCTGGGAGTGTCCGAGGGGCCTGGCCCAGGATCT
AGCGTCTTTAATGTGGTCAACTCCTCTATTGGGCTCATCATGGGACCCGGACCTGGGGTGAAA
AATGTCATTGGCCCATTCATGAAGGCCGTGTGTGTCGAAGGACCCGGGCCTGGCATGAACTAC
TATGGAAAGCAAGAAAATTGGTACAGCCTGAAGAAAGGCCCTGGGCCAGGCGGACTGGCTTA
CAAGTTTGTGGTCCCAGGGGCAGCCACTCCCTATGGGCCTGGGCCAGGCCCCGATTCCATCCA
GGACTCTCTCAAAGAGAGCCGGAAACTGAACGGACCCGGGCCTGGACTGCTCATTTTCCACAT
CAATGGCAAAATTATCAAGAACAGCGAGGGACCTGGGCCAGGCGCCGGACTGCTGGGGAACG
TGTCCACCGTCCTGCTCGGCGGAGTGGGGCCCGGCCCTGGGAAGTACAAGATCGCTGGAGGG
ATCGCAGGCGGACTGGCCCTGCTGGGCCCAGGACCAGGGATGCGCAAACTGGCTATTCTCTCT
GTCTCCAGCTTTCTGTTTGTGTGA

FIGURE 18N

Protein	Sequence	Restriction
HIV gag 386	VLAEAMSQV	HLA-A2
HIV gag 271	MTNNPPIPV	HLA-A2
HIV pol 774	MASDFNLPPV	HLA-A2
HIV pol 448	KLVGKLNWA	HLA-A2
HIV pol 163	LVGPTPVNI	HLA-A2
HIV pol 498	ILKEPVHGV	HLA-A2
HIV pol 879	KAACWWAGI	HLA-A2
HIV pol 132	KMIGGIGGFI	HLA-A2
HIV pol 772	RAMASDFNL	HLA-A2
HIV pol 183	TLNFPISPI	HLA-A2
HIV env 184	KLTPLCVTL	HLA-A2
HIV env 651	LLQLTVWGI	HLA-A2
HIV env 163	SLLNATDIAV	HLA-A2
HIV nef 221	LTFGWCFKL	HLA-A2
HIV vpr 59	AIIRILQQL	HLA-A2
HIV vpr 62	RILQQLLFI	HLA-A2
HIV pol 929	QMAVFIHNFK	HLA-A3
HIV pol 722	KVYLAWVPAHK	HLA-A3
HIV pol 971	KIQNFRVYYR	HLA-A3
HIV pol 347	AIFQSSMTK	HLA-A3
HIV pol 98	VTIKIGGQLK	HLA-A3
HIV env 61	TTLFCASDAK	HLA-A3
HIV env 47	VTVYYGVPVWK	HLA-A3
HIV nef 100	QVPLRPMTYK	HLA-A3
HIV vif 7	VMIVWQVDR	HLA-A3
HIV gag 162	QMVHQAISPR	HLA-A3
HIV gag 545	YPLASLRSLF	HLA-B7
HIV gag 237	HPVHAGPIA	HLA-B7
HIV pol 186	FPISPIETV	HLA-B7
HIV pol 893	IPYNPQSQGVV	HLA-B7
HIV env 259	IPIHYCAPA	HLA-B7
HIV env 250	CPKVSFEPI	HLA-B7
HIV nef 94	FPVRPQVPL	HLA-B7
HIV rev 75	VPLQLPPL	HLA-B7
HIV pol 684	EVNIVTDSQY	HLA-A1
HIV gag 317	FRDYVDRFY	HLA-A1
HIV pol 368	VIYQYMDDLY	HLA-A1
HIV pol 295	VTVLDVGDAY	HLA-A1
HIV pol 533	IYQEPFKNL	HLA-A24
HIV pol 244	PYNTPVFAI	HLA-A24
HIV pol 530	TYQIYQEPF	HLA-A24
HIV pol 597	YWQATWIPEW	HLA-A24
HIV env 681	IWGCSGKLI	HLA-A24
HIV env 671	RYLKDQQLL	HLA-A24

FIGURE 19A

Protein	Sequence	Restriction
HIV env 55	VWKEATTTLF	HLA-A24
HIV vpr 46	IYETYGDTW	HLA-A24
HIV vpr 14	PYNEWTLEL	HLA-A24
HIV gag 298	KRWIILGLNKIVRMY	HLA-DR
HIV pol 596	WEFVNTPPLVKLWYQ	HLA-DR
HIV pol 956	QKQITKIQNFRVYYR	HLA-DR
HIV pol 712	KVYLAWVPAHKGIGG	HLA-DR
HIV gag 294	GEIYKRWIILGLNKI	HLA-DR
HIV pol 711	EKVYLAWVPAHKGIG	HLA-DR
HIV env 729	QHLLQLTVWGIKQLQ	HLA-DR
HIV gag 171	QGQMVHQAISPRTLN	HLA-DR
HIV pol 835	SPAIFQSSMTKILEP	HLA-DR
HIV env 566	IKQFINMWQEVGKAMY	HLA-DR
HIV pol 303	FRKYTAFTIPSINNE	HLA-DR
HIV pol 758	HSNWRAMASDFNLPP	HLA-DR
HIV pol 915	KTAVQMAVFIHNFKR	HLA-DR
HIV vpu 31	YRKILRQRKIDRLID	HLA-DR3
HIV pol 874	WAGIKQEFGIPYNPQ	HLA-DR3
HIV pol 674	EVNIVTDSQYALGII	HLA-DR3
HIV pol 619	AEIFYVDGAANRETK	HLA-DR3
HIV pol 989	GAVVIQDNSDIKVVP	HLA-DR3
HCV NS4 1812	LLFNILGGWV	HLA-A2
HCV NS1/E2 728	FLLLADARV	HLA-A2
HCV NS4 1590	YLVAYQATV	HLA-A2
HCV NS5 2611	RLIVFPDLGV	HLA-A2
HCV CORE 132	DLMGYIPLV	HLA-A2
HCV NS4 1920	WMNRLIAFA	HLA-A2
HCV NS4 1666	VLVGGVLAA	HLA-A2
HCV NS4 1769	HMWNFISGI	HLA-A2
HCV NS4 1851	ILAGYGAGV	HLA-A2
HCV CORE 35	YLLPRRGPRL	HLA-A2
HCV NS1/E2 726	LLFLLLADA	HLA-A2
HCV LORF 1131	YLVTRHADV	HLA-A2
HCV CORE 51	KTSERSQPR	HLA-A3
HCV CORE 43	RLGVRATRK	HLA-A3
HCV ENV1 290	QLFTFSPRR	HLA-A3
HCV NS1/E2 632	RMYVGGVEHR	HLA-A3
HCV NS3 1396	LIFCHSKKK	HLA-A3
HCV NS4 1863	GVAGALVAFK	HLA-A3
HCV NS4 1864	VAGALVAFK	HLA-A3
HCV NS3 1262	LGFGAYMSK	HLA-A3
HCV Core 169	LPGCSFSIF	HLA-B7
HCV NS5 2922	LSAFSLHSY	HLA-A1
HCV NS3 1128	CTCGSSDLY	HLA-A1
HCV NS5 2180	LTDPSHITA	HLA-A1

FIGURE 19B

Protein	Sequence	Restriction
HCV Core 126	LTCGFADLMGY	HLA-A1
HCV NS3 1305	LADGGCSGGAY	HLA-A1
HCV NS4 1765	FWAKHMWNF	HLA-A24
HCV NS5 2875	RMILMTHFF	HLA-A24
HCV NS5 2639	VMGSSYGF	HLA-A24
HCV NS4 1765	FWAKHMWNFI	HLA-A24
P. falciparum SSP2-230	FMKAVCVEV	HLA-A2
P. falciparum EXP1-83	GLLGVVSTV	HLA-A2
P. falciparum CSP-7	ILSVSSFLFV	HLA-A2
P. falciparum LSA1-94	QTNFKSLLR	HLA-A3
P. falciparum LSA1-105	GVSENIFLK	HLA-A3
P. falciparum SSP2-522	LLACAGLAYK	HLA-A3
P. falciparum SSP2-539	TPYAGEPAPF	HLA-B7
P. falciparum LSA1-1663	LPSENERGY	HLA-A1
P. falciparum EXP1-73	KYKLATSVL	HLA-A24
P. falciparum CSP-12	SFLFVEALF	HLA-A24
P. falciparum LSA1-10	YFILVNLLI	HLA-A24
P. falciparum SSP2-14	FLIFFDLFLV	HLA-A2
P. falciparum EXP1-80	VLAGLLGVV	HLA-A2
P. falciparum EXP1-91	VLLGGVGLVL	HLA-A2
P. falciparum SSP2-523	LACAGLAYK	HLA-A3
P. falciparum EXP1-10	ALFFILFNK	HLA-A3
P. falciparum LSA1-11	FILVNLLIFH	HLA-A3
P. falciparum SSP2-126	LPYGRTNL	HLA-B7
P. falciparum CSP-15	FVEALFQEY	HLA-A1
P. falciparum LSA1-1794	FQDEENIGIY	HLA-A1
P. falciparum LSA1-9	FYFILVNLL	HLA-A24
P. falciparum SSP2-8	KYLVIVFLI	HLA-A24
P. falciparum CSP-394	GLIMVLSFL	HLA-A2
P. falciparum EXP1-2	KILSVFFLA	HLA-A2
P. falciparum CSP-344	VTCGNGIQVR	HLA-A3
P. falciparum LSA1-59	HVLSHNSYEK	HLA-A3
P. falciparum SSP2-207	PSDGKCNLY	HLA-A1
P. falciparum LSA1-1671	YYIPHQSSL	HLA-A24
P. falciparum LSA1-1876	KFIKSLFHIF	HLA-A24
P. falciparum SSP2-13	VFLIFFDLFL	HLA-A24
P. falciparum LSA1-1881	LFHIFDGDNEI	HLA-A24
P. falciparum CSP-55	YYGKQENWYSL	HLA-A24
P. falciparum LSA1-5	LYISFYFI	HLA-A24
P. falciparum CSP-2	MRKLAILSVSSFLFV	HLA-DR
P. falciparum CSP-53	MNYYGKQENWYSLKK	HLA-DR
P. falciparum CSP-375	SSVFNVVNSSIGLIM	HLA-DR
P. falciparum SSP2-61	RHNWVNHAVPLAMKLI	HLA-DR
P. falciparum SSP2-165	PDSIQDSLKESRKLN	HLA-DR3
P. falciparum SSP2-211	KCNLYADSAWENVKN	HLA-DR3

FIGURE 19C

Protein	Sequence	Restriction
P. falciparum SSP2-223	VKNVIGPFMKAVCVE	HLA-DR
P. falciparum SSP2-509	KYKIAGGIAGGLALL	HLA-DR
P. falciparum SSP2-527	GLAYKFVVPGAATPY	HLA-DR
P. falciparum EXP1-71	KSKYKLATSVLAGLL	HLA-DR
P. falciparum EXP1-82	AGLLGNVSTVLLGGV	HLA-DR
P. falciparum LSA1-16	LLIFHINGKIIKNSE	HLA-DR
P. falciparum LSA1-94	QTNFKSLLRNLGVSE	HLA-DR
HBV core 18	FLPSDFFPSV	HLA-A2
HBV env 183	FLLTRILTI	HLA-A2
HBV env 335	WLSLLVPFV	HLA-A2
HBV pol 455	GLSRYVARL	HLA-A2
HBV pol 538	YMDDVVLGV	HLA-A2/A1
HBV pol 773	ILRGTSFVYV	HLA-A2
HBV pol 562	FLLSLGIHL	HLA-A2
HBV pol 642	ALMPLYACI	HLA-A2
HBV env 338	GLSPTVWLSV	HLA-A2
HBV core 141	STLPETTVVRR	HLA-A3
HBV pol 149	HTLWKAGILYK	HLA-A3/A1
HBV pol 150	TLWKAGILYK	HLA-A3
HBV pol 388	LVVDFSQFSR	HLA-A3
HBV pol 47	NVSIPWTHK	HLA-A3
HBV pol 531	SAICSVVRR	HLA-A3
HBV pol 629	KVGNFTGLY	HLA-A3/A1
HBV pol 665	QAFTFSPTYK	HLA-A3
HBV core 19	LPSDFFPSV	HLA-B7
HBV env 313	IPIPSSWAF	HLA-B7
HBV pol 354	TPARVTGGVF	HLA-B7
TB	RMSRVTTFTV	HLA-A2
TB	ALVLLMLPVV	HLA-A2
TB	LMIGTAAAVV	HLA-A2
TB	ALVLLMLPV	HLA-A2
TB	GLMTAVYLV	HLA-A2
TB	MALLRLPV	HLA-A2
TB	RMFAANLGV	HLA-A2
TB	SLYFGGICV	HLA-A2
TB	RLPLVLPAV	HLA-A2
TB	RLMIGTAAA	HLA-A2
TB	FVVALIPLV	HLA-A2
TB	MTYAAPLFV	HLA-A2
TB	AMALLRLFLV	HLA-A2
p53 139	KLCPVQLWV	HLA-A2
CEA 687	ATVGIMIGV	HLA-A2
CEA 691	IMIGHLVGV	HLA-A2
Her2/neu 689	RLLQETELV	HLA-A2
MAGE3 112	KVAEIVHFL	HLA-A2

FIGURE 19D

Protein	Sequence	Restriction
Her2/neu 665	VVLGVVFGI	HLA-A2
p53 149	SMPPPGTRV	HLA-A2
PAP.21.T2	LTFFWLDRSV	HLA-A2
PAP.112	TLMSAMTNL	HLA-A2
PAP.284	IMYSAHDTTV	HLA-A2
PSM.288.V10	GLPSIPVHPV	HLA-A2
PSM.441	LLQERGVAYI	HLA-A2
PSM.469L2	LLYSLVHNL	HLA-A2
PSM.663	MMNDQLMFL	HLA-A2
PSA.3.V11	FLTLSVTWIGV	HLA-A2
PSA.143.V8	ALGTTCYV	HLA-A2
PSA.161	FLTPKKLQCV	HLA-A2
HuK2.4.L2	LLLSIALSV	HLA-A2
HuK2.53.V11	VLVHPQWVLTV	HLA-A2
HuK2.165	FLRPRSLQCV	HLA-A2
HuK2.216.V11	PLVCNGVLQGV	HLA-A2

FIGURE 19E

Figure 20A

ID#	Epitope	Sequence	Conservation	HLA restriction	Prototype Binding	XRN[1]
924.07	core 18	FLPSDFFPSV	45	A2	3.5	5
777.03	env 183	FLLTRILTI	80	A2	9.8	4
1013.01	env 335	WLSLLVPFV	100	A2	5.4	4
1168.02	pol 455	GLSRYVARL	55	A2	55.9	3
1090.77	pol 538	YMDDVVLGV	90	A2/A1	6.4	5
927.11	pol 562	FLLSLGIHL	95	A2	7.8	3
927.15	pol 642	ALMPLYACI	95	A2	12.9	4
1083.01	core 141	STLPETTVVRR	95	A3/A11	735 / 4.5	4
1147.16	pol 149	HTLWKAGILYK	100	A3/A1	15.4 / 15.6	5
1069.15	pol 150	TLWKAGILYK	100	A3/A11	2.1 / 33	2
1069.20	pol 388	LVVDFSQFSR	100	A3/A11	6875 / 17	3
1069.16	pol 47	NVSIPWTHK	100	A3/A11	174 / 117	3
1090.11	pol 531	SAICSVVRR	95	A3/A11	2189 / 29	3
1142.05	pol 629	KVGNFTGLY	95	A3/A1	58 / 365	2
1090.10	pol 665	QAFTFSPTYK	95	A3/A11	249 / 8	3
988.05	core 19	LPSDFFPSV	45	B7	3026.8	4
1145.04	env 313	IPIPSSWAF	100	B7	42.3	4
1147.04	pol 354	TPARVTGGVF	90	B7	13.2	2
1147.02	pol 429	HPAAMPHLL	100	B7	56.6	4
1039.06	env 359	WMMWYWGPSLY	85	A1	16.3	3
1448.01	core 419	DLLDTASALY	75	A1	2.3	3
1373.88	core 137	LTFGRETVLEY	75	A1	80.0	3
1090.07	pol 415	LSLDVSAAFY	95	A1	6.0	3
20.0271	pol 392	SWPKFAVPNL	95	A24	2.1	2
1373.56	env 332	RFSWLSLLVPF	100	A24	12.0	2
1373.07	core 117	EYLVSFGVW	90	A24	16.0	2
1069.23	pol 745	KYTSFPWLL	85	A24	1.0	3

[1]XRN = Cross binding, number of HLA types in the supertype panel of 5 for which significant binding as detected

Figure 20B

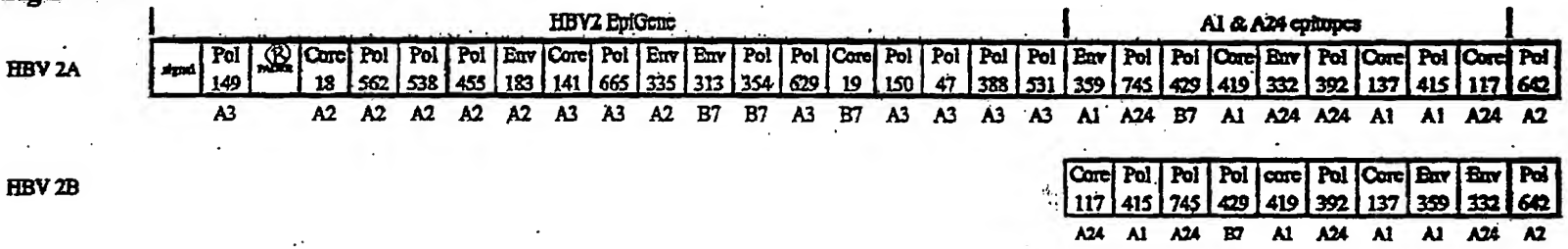

HBV2 EpiGenic
A1 & A24 epitopes
HBV 2A
Pol 149 A3
Core 18 A2
Pol 562 A2
Pol 538 A2
Pol 455 A2
Env 183 A2
Core 141 A3
Pol 665 A3
Env 335 A2
Env 313 B7
Pol 354 B7
Pol 629 A3
Core 19 B7
Pol 150 A3
Pol 47 A3
Pol 388 A3
Pol 531 A3
Env 359 A1
Pol 745 A24
Pol 429 B7
Core 419 A1
Env 332 A24
Pol 392 A24
Core 137 A1
Pol 415 A1
Core 117 A24
Pol 642 A2
HBV 2B
Core 117 A24
Pol 415 A1
Pol 745 A24
Pol 429 B7
core 419 A1
Pol 392 A24
Core 137 A1
Env 359 A1
Env 332 A24
Pol 642 A2

Figure 20C

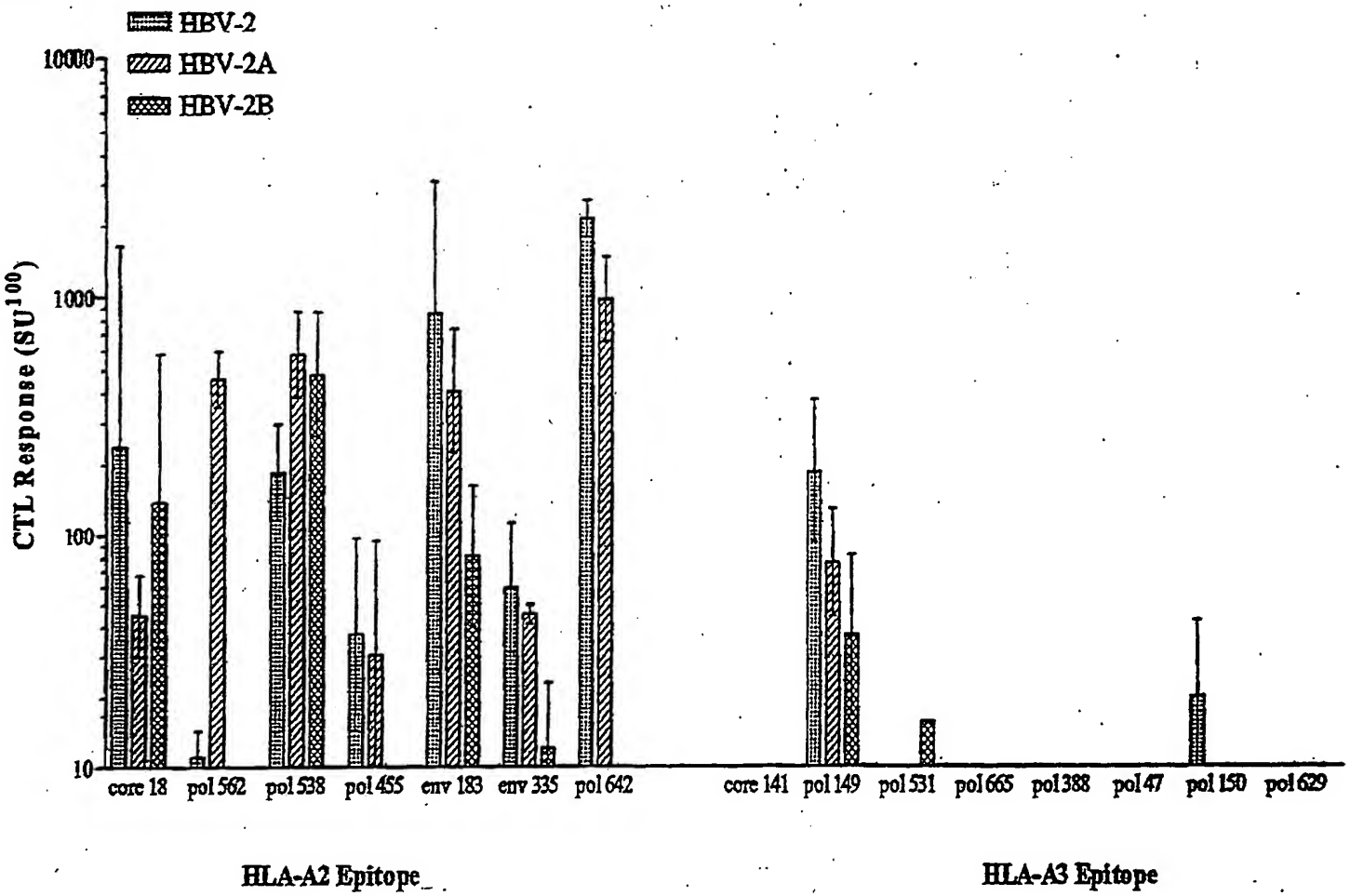

HBV-2
HBV-2A
HBV-2B
10000
1000
100
10
CTL Response (SU/100)
core 18
pol 562
pol 538
pol 455
env 183
env 335
pol 642
core 141
pol 149
pol 531
pol 665
pol 388
pol 47
pol 150
pol 629
HLA-A2 Epitope
HLA-A3 Epitope

Figure 20D

HBV-2

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVNFLLSLGIHLYMDDVVL
GVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWLSLLVPFVNIPIPSSWAFKTPARVTGG
VFKVGNFTGLYNLPSDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVDFSQFSRNSAICSVVRRALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCC
TGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCTGCC
TAGCGATTTCTTTCCTAGCGTGAACTTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGCTG
GGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAG
AGACCACCGTGGTGAGGAGGCAGGCCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCT
GCTGGTGCCCTTTGTGAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGACCGGAGGA
GTGTTTAAGGTGGGAAACTTCACCGGCCTGTATAACCTGCCCAGCGATTTCTTTCCTAGCGTGAAGACCCTGT
GGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCGCTCTGGTGGTGGACTT
TTCCCAGTTCAGCAGAAATTCCGCTATCTGCTCCGTGGTGAGGAGAGCTCTGATGCCACTGTATGCCTGTATC
TGA

Figure 20E

HBV-2A

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVNFLLSLGIHLYMDDVVL
GVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWLSLLVPFVNIPIPSSWAFKTPARVTGG
VFKVGNFTGLYNLPSDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVDFSQFSRNSAICSVVRRKAWMMWYWG
PSLYKKYTSFPWLLNAHPAAMPHLLKAAADLLDTASALYNAAARFSWLSLLVPFNAASWPKFAVPNLKLTFGR
ETVLEYKALSLDVSAAFYGAAEYLVSFGVWGAALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCC
TGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCTGCC
TAGCGATTTCTTTCCTAGCGTGAACTTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGCTG
GGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAG
AGACCACCGTGGTGAGGAGGCAGGCCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCT
GCTGGTGCCCTTTGTGAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGACCGGAGGA
GTGTTTAAGGTGGGAAACTTCACCGGCCTGTATAACCTGCCCAGCGATTTCTTTCCTAGCGTGAAGACCCTGT
GGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCGCTCTGGTGGTGGACTT
TTCCCAGTTCAGCAGAAATAGCGCCATCTGTTCGGTCGTGAGAAGGAAAGCCTGGATGATGTGGTACTGGGGT
CCTAGTCTGTATAAGAAGTACACCTCATTCCCATGGCTCTTGAATGCCCATCCCGCTGCAATGCCACACCTGC
TTAAAGCTGCGGCGGATCTGCTGGACACAGCCTCAGCTTTATATAATGCTGCAGCAAGATTCTCCTGGTTGTC
TCTCTTAGTGCCCTTCAACGCAGCTTCCTGGCCAAAATTTGCCGTTCCGAACCTGAAGCTCACTTTTGGAAGA
GAGACAGTACTTGAATACAAAGCACTAAGCCTTGACGTGTCAGCAGCCTTCTACGGAGCAGCAGAATATCTAG
TATCTTTTGGGGTCTGGGGCGCAGCCCTCATGCCTCTATACGCCTGCATTTGA

Figure 20F

HBV-2B

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPSDFFPSVNFLLSLGIHLYMDDVVL
GVGLSRYVARLFLLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWLSLLVPFVNIPIPSSWAFKTPARVTGG
VFKVGNFTGLYNLPSDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVDFSQFSRNSAICSVVRRKEYLVSFGV
WGLSLDVSAAFYNAAAKYTSFPWLLNAHPAAMPHLLKAAADLLDTASALYNSWPKFAVPNLKLTFGRETVLEY
KAAWMMWYWGPSLYKAAARFSWLSLLVPFGAAALMPLYACI

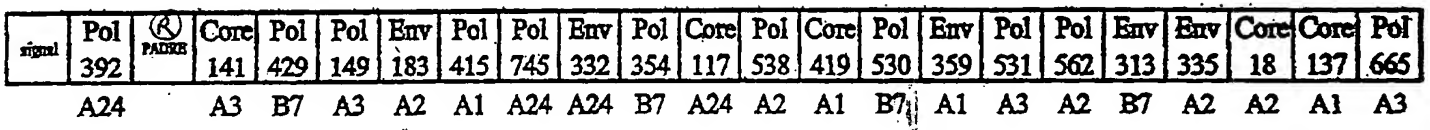
ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCC
TGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTGAAGGCTGCCGCTTTCCTGCC
TAGCGATTTCTTTCCTAGCGTGAACTTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGCTG
GGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAG
AGACCACCGTGGTGAGGAGGCAGGCCTTCACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCT
GCTGGTGCCCTTTGTGAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCCAGCCAGGGTGACCGGAGGA
GTGTTTAAGGTGGGAAACTTCACCGGCCTGTATAACCTGCCCAGCGATTTCTTTCCTAGCGTGAAGACCCTGT
GGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCGCTCTGGTGGTGGACTT
TTCCCAGTTCAGCAGAAATTCAGCAATTTGTTCGGTGGTGAGAAGAAAGGAATATCTTGTTTCATTTGGCGTC
TGGGGGCTGTCACTGGATGTAAGTGCGGCATTTTACAATGCCGCCGCAAAATATACAAGCTTCCCATGGCTCC
TAAACGCACACCCAGCTGCAATGCCGCATCTACTGAAAGCAGCCGCTGACCTCTTAGACACTGCCTCCGCTCT
GTACAACTCTTGGCCCAAGTTTGCCGTGCCTAATCTCAAGTTGACCTTCGGTAGAGAGACAGTCTTAGAATAC
AAAGCGGCCTGGATGATGTGGTACTGGGGACCCTCTCTGTATAAAGCCGCTGCAAGGTTCTCCTGGCTTAGCC
TTCTCGTACCATTCGGAGCAGCTGCCCTAATGCCTTTGTACGCATGCATCTGA

Figure 21A

ID#	Epitope	Sequence	Conservation	HLA restriction	Prototype Binding	XRN
924.07	core 18	FLPSDFFPSV	45	A2	3.5	5
777.03	env 183	FLLTRILTI	80	A2	9.8	4
1013.01	env 335	WLSLLVPFV	100	A2	5.4	4
927.11	pol 562	FLLSLGIHL	95	A2	7.8	3
1090.77	pol 538	YMDDVVLGV	90	A2/A1	6.4	5
1083.01	core 141	STLPETTVVRR	95	A3/A11	735 / 4.5	4
1147.16	pol 149	HTLWKAGILYK	100	A3/A1	15.4 / 15.6	5
1090.11	pol 531	SAICSVVRR	95	A3/A11	2189 / 29	3
1090.10	pol 665	QAFTFSPTYK	95	A3/A11	249 / 8	3
1145.04	env 313	IPIPSSWAF	100	B7	42.3	4
1147.04	pol 354	TPARVTGGVF	90	B7	13.2	2
1147.02	pol 429	HPAAMPHLL	100	B7	56.6	4
1147.05	pol 530	FPHCLAFSYM	95	B7	58.5	5
1039.06	env 359	WMMWYWGPSLY	85	A1	16.3	3
1448.01	core 419	DLLDTASALY	75	A1	2.3	3
1373.88	core 137	LTFGRETVLEY	75	A1	80.0	3
1090.07	pol 415	LSLDVSAAFY	95	A1	6.0	3
20.0271	pol 392	SWPKFAVPNL	95	A24	2.1	2
1373.56	env 332	RFSWLSLLVPF	100	A24	12.0	2
1373.07	core 117	EYLVSFGVW	90	A24	16.0	2
1069.23	pol 745	KYTSFPWLL	85	A24	1.0	3

Figure 21B

HBV 21A



HBV 21B

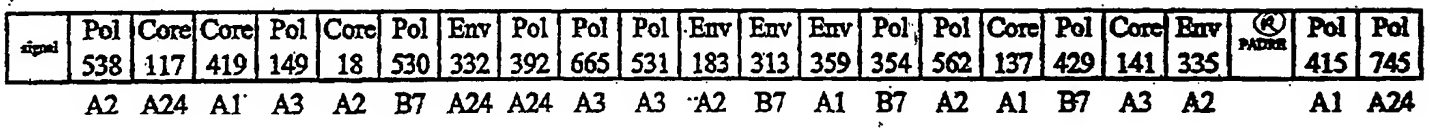
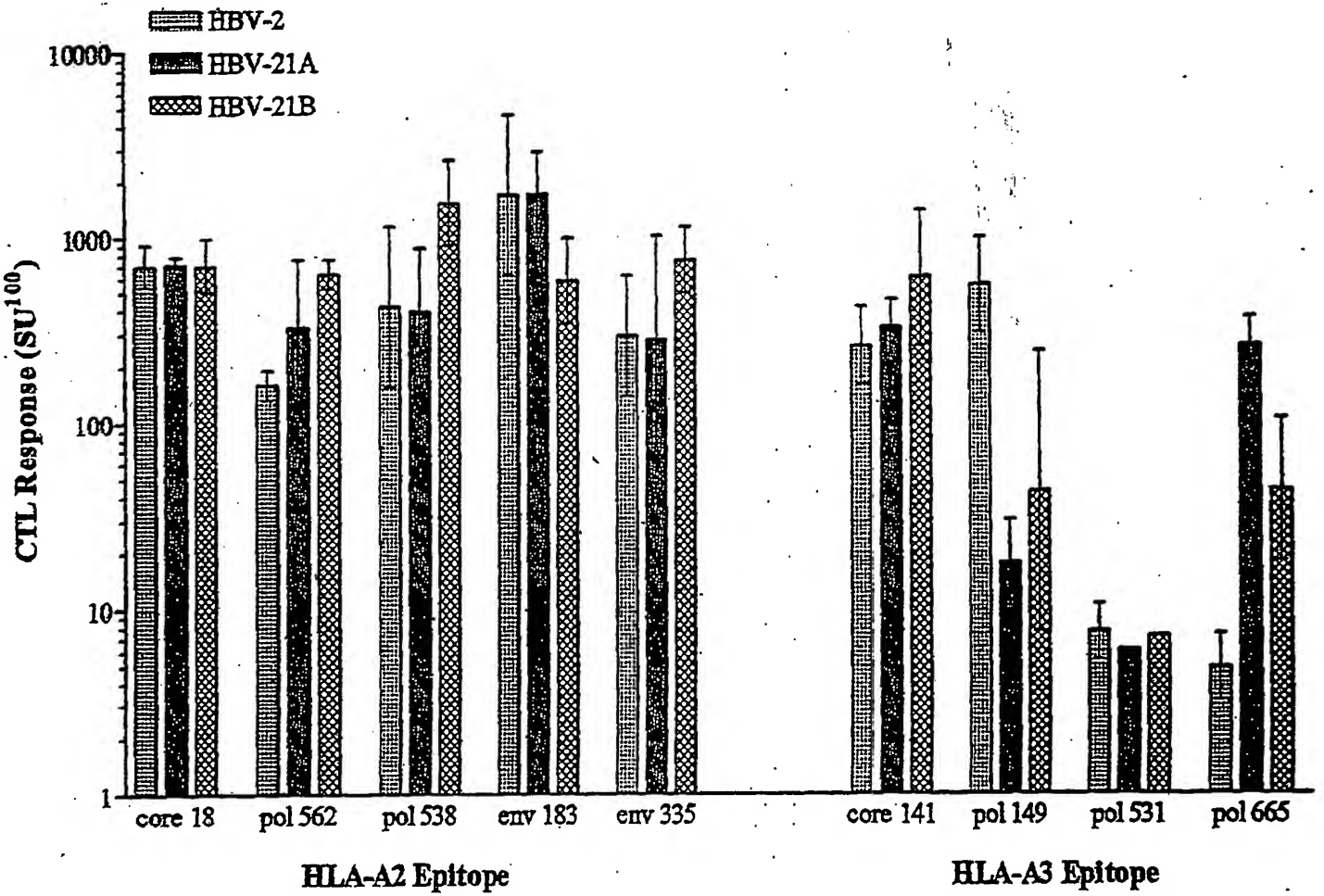


Figure 21C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HBV-21A
HBV-21B
10000
1000
100
10
1
CTL Response (SU100)
core 18
pol 562
pol 538
env 183
env 335
core 141
pol 149
pol 531
pol 665
HLA-A2 Epitope
HLA-A3 Epitope

Figure 21D

HBV-21A

MGMQVQIQSLFLLLLWVPGSRGSWPKFAVPNLKAAAAKFVAAWTLKAAAKSTLPETTVVRRKHPAAMPHLLKA
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AICSVVRRKNFLLSLGIHLNIPIPSSWAFKAAWLSLLVPFVNAFLPSDFFPSVKLTFGRETVLEYKQAFTFSP
TYK

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TAAGAGCACACTGCCAGAGACCACCGTGGTCCGGCGAAAGCATCCAGCCGCAATGCCCCACTTGCTCAAAGCA
GCCGCCCACACTCTTTGGAAGGCTGGGATATTGTACAAGAAAGCCTTCCTTCTGACCAGGATATTAACTATCG
GAGCTCTGTCACTCGACGTTTCTGCTGCCTTCTACAACGCGGCGGCAAAATACACTAGCTTTCCATGGCTACT
CAACGCAGCCGCCAGATTTTCTTGGCTATCACTACTGGTGCCATTTAATGCAGCAACACCTGCTAGAGTGACT
GGCGGCGTCTTTAAAGCAGCCGAGTACTTGGTGAGCTTTGGCGTCTGGGGTGCAGCGGCATATATGGATGATG
TAGTGTTAGGGGTGAACGACCTCCTGGACACAGCCAGTGCGCTGTACAATGCAGCTGCATTCCCGCATTGCCT
AGCCTTCAGTTATATGAAAGCAGCAGCCTGGATGATGTGGTACTGGGGACCGTCCCTTTATAAAGCAGCTTCA
GCAATCTGTTCCGTTGTGAGGAGAAAAAACTTTTTACTCTCCCTCGGTATTCACCTGAACATTCCCATCCCTT
CCTCATGGGCATTCAAAGCCGCTTGGCTGAGTCTACTCGTACCTTTCGTTAATGCATTTCTGCCCAGCGACTT
TTTCCCCTCGGTAAAACTGACATTCGGACGCGAAACAGTCCTTGAATATAAGCAGGCCTTCACGTTCTCACCA
ACCTATAAATGA

Figure 21E

HBV-21B

MGMQVQIQSLFLLLLWVPGSRGYMDDVVLGVNAAAEYLVSFGVWNDLLDTASALYGAAHTLWKAGILYKKAFL
PSDFFPSVKAFPHCLAFSYMKAARFSWLSLLVPFNAASWPKFAVPNLKAAAQAFTFSPTYKNAAASAICSVVR
RKAFLLTRILTINIPIPSSWAFKAAWMMWYWGPSLYKAAATPARVTGGVFKAANFLLSLGIHLNLTFGRETVL
EYKHPAAMPHLLKAASTLPETTVVRRKWLSLLVPFVNAAAAKFVAAWTLKAAAKLSLDVSAAFYNAAAKYTSF
PWLL

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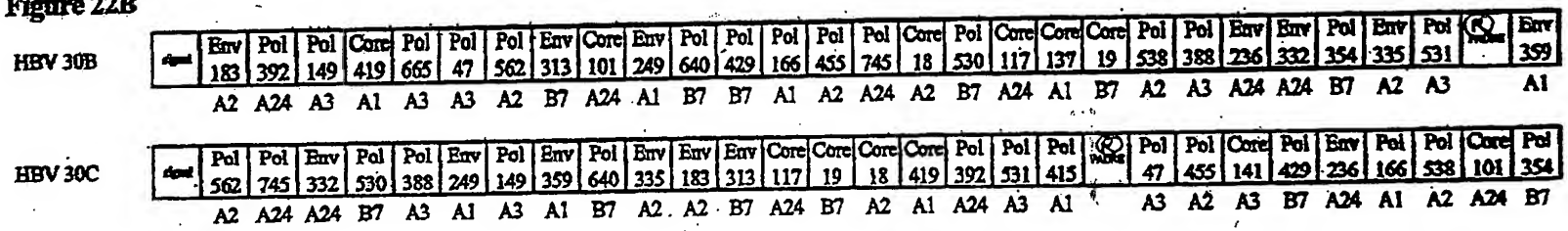
CACTGCATCTGCTCTGTACGGTGCAGCCCATACCCTGTGGAAGGCCGGAATCCTCTACAAAAAGGCATTCCTA
CCTAGCGACTTTTTTCCTTCAGTGAAAGCCTTCCCACATTGCCTAGCATTCTCGTATATGAAAGCGGCTAGGT
TCTCATGGCTTAGTCTTCTAGTACCTTTCAATGCCGCCTCCTGGCCCAAATTCGCCGTACCAAATCTAAAAGC
GGCCGCGCAGGCCTTTACATTCTCTCCGACTTATAAAAATGCAGCAGCCTCCGCTATTTGTAGCGTCGTGCGC
CGAAAGGCCTTCCTGCTAACCCGGATTTTGACGATAAACATCCCCATCCCTTCTAGCTGGGCTTTCAAAGCAG
CATGGATGATGTGGTACTGGGGTCCCAGCTTATACAAAGCTGCGGCAACCCCAGCAAGAGTGACAGGGGGCGT
GTTTAAGGCCGCCAACTTCCTCCTGAGTCTCGGAATACACCTGAACTTAACCTTTGGGAGAGAGACAGTACTG
GAGTATAAACACCCAGCAGCTATGCCGCACCTACTCAAAGCCGCTTCAACACTCCCAGAAACAACTGTAGTGA
GGAGAAAATGGCTCTCCCTGCTTGTCCCATTTGTCAACGCCGCCGCCGCTAAGTTTGTGGCCGCTTGGACACT
TAAGGCTGCAGCAAAGTTGTCACTTGATGTTAGTGCAGCGTTCTATAACGCAGCTGCAAAATACACTTCCTTT
CCCTGGCTGCTGTGA

Figure 22A

ID#	Epitope	Sequence	Conservation	HLA restriction	Prototype Binding	XRN
924.07	core 18	FLPSDFFPSV	45	A2	3.5	5
777.03	env 183	FLLTRILTI	80	A2	9.8	4
1013.01	env 335	WLSLLVPFV	100	A2	5.4	4
1168.02	pol 455	GLSRYVARL	55	A2	55.9	3
1090.77	pol 538	YMDDVVLGV	90	A2/A1	6.4	5
927.11	pol 562	FLLSLGIHL	95	A2	7.8	3
1083.01	core 141	STLPETTVVRR	95	A3/A11	735 / 4.5	4
1147.16	pol 149	HTLWKAGILYK	100	A3/A1	15.4 / 15.6	5
1069.20	pol 388	LVVDPSQFSR	100	A3/A11	6875 / 17	3
1069.16	pol 47	NVSIPWTHK	100	A3/A11	174 / 117	3
1090.11	pol 531	SAICSVVRR	95	A3/A11	2189 / 29	3
1090.10	pol 665	QAFTFSPTYK	95	A3/A11	249 / 8	3
988.05	core 19	LPSDFFPSV	45	B7	3026.8	4
1145.04	env 313	IPIPSSWAF	100	B7	42.3	4
1147.04	pol 354	TPARVTGGVF	90	B7	13.2	2
1147.02	pol 429	HPAAMPHLL	100	B7	56.6	4
1147.05	pol 530	FPHCLAFSYM	95	B7	58.5	5
1359.01	pol 640	YPALMPLYACI	95	B7	1393.4	3
1039.06	env 359	WMMWYWQPSLY	85	A1	16.3	3
1448.01	core 419	DLLDTASALY	75	A1	2.3	3
1373.88	core 137	LTFGRETVLEY	75	A1	80.0	3
1373.78	pol 166	ASFCGSPY	100	A1	247.0	3
1090.07	pol 415	LSLDVSAAFY	95	A1	6.0	3
1069.08	env 249	ILLLCLIFLL	100	A1	192.0	1
20.0269	env 236	RWMCLRRFII	95	A24	11.0	3
20.0271	pol 392	SWPKFAVPNL	95	A24	2.1	2
1373.56	env 332	RFSWLSLLVPF	100	A24	12.0	2
1373.38	core 101	LWFHISCLTF	85	A24	6.7	3
1373.07	core 117	EYLVSFGVW	90	A24	16.0	2
1069.23	pol 745	KYTSFPWLL	85	A24	1.0	3

Figure 22B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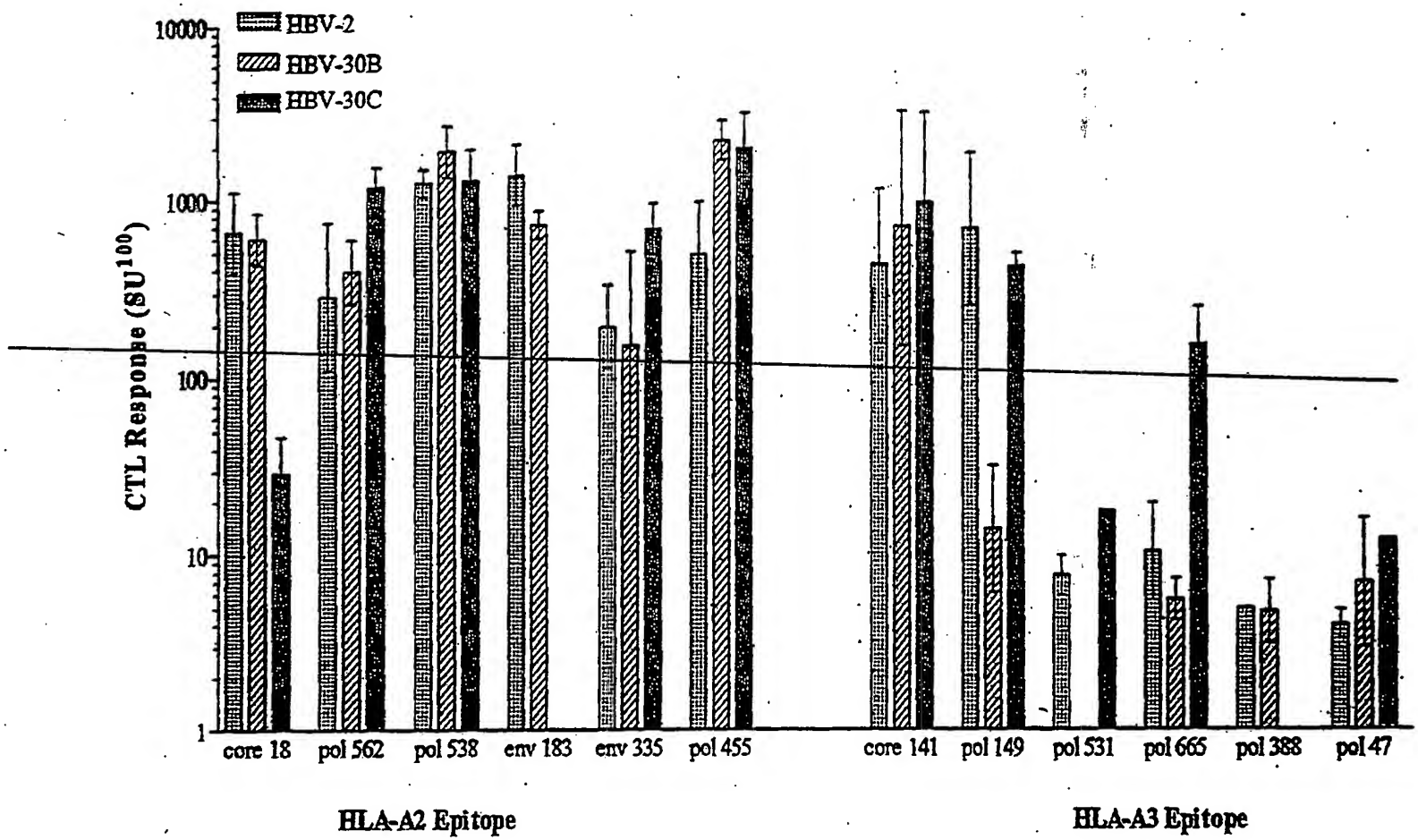
A2 A24 A3 A1 A3 A3 A2 B7 A24 A1 B7 B7 A1 A2 A24 A2 B7 A24 A1 B7 A2 A3 A24 A24 B7 A2 A3 A1
HBV 30C
Pol 562 Pol 745 Env 332 Pol 530 Pol 388 Env 249 Pol 149 Env 359 Pol 640 Env 335 Env 183 Env 313 Core 117 Core 19 Core 18 Core 419 Pol 392 Pol 531 Pol 415 Pol 47 Pol 455 Core 141 Pol 429 Env 236 Pol 166 Pol 538 Core 101 Pol 354
A2 A24 A24 B7 A3 A1 A3 A1 B7 A2 A2 B7 A24 B7 A2 A1 A24 A3 A1 A3 A2 A3 B7 A24 A1 A2 A24 B7

Figure 22C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HBV-30B
HBV-30C
10000
1000
100
10
1
CTL Response (SU100)
core 18
pol 562
pol 538
env 183
env 335
pol 455
core 141
pol 149
pol 531
pol 665
pol 388
pol 47
HLA-A2 Epitope
HLA-A3 Epitope

Figure 22D

HBV-30B

MGMQVQIQSLFLLLLWVPGSRGFLLTRILTINAAASWPKFAVPNLKAAAHTLWKAGILYKKADLLDTASALYN
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FPHCLAFSYMKAEYLVSFGVWNAALTFGRETVLEYKAAALPSDFFPSVKAYMDDVVLGVNLVVDFSQFSRNAA
ARWMCLRRFIINAARFSWLSLLVPFNAATPARVTGGVFKAAWLSLLVPFVNSAICSVVRRKAKFVAAWTLKAA
AKWMMWYWGPSLYKAASTLPETTVVRRKLSLDVSAAFY

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CAGGCTTTTACTTTCTCTCCTACATATAAAGGCGCAGCTGCAAACGTGAGTATCCCTTGGACGCACAAAGGAG
CCGCTGCCAACTTCTTACTGTCCCTGGGCATCCATCTAAATATCCCTATTCCTTCATCCTGGGCATTTAAAGC
AGCCGCCTTATGGTTCCACATAAGTTGTCTGACCTTCAAAGCCGCAGCAATCCTGCTCCTTTGCCTCATTTTC
TTACTAAACGCCGCTGCCTATCCAGCTCTTATGCCATTGTACGCATGTATCAACGCCCACCCCGCAGCAATGC
CCCACCTCCTTAAAGCTGCCGCCAGTTTCTGCGGTTCTCCTTATAAAGCAGCAGGGCTGTCCAGATACGTAGC
TAGGCTAAACAAGTATACCAGCTTCCCCTGGTTACTTAATTTCCTGCCGTCAGATTTCTTTCCATCAGTTAAG
GCCTTCCCTCATTGTCTGGCCTTTAGCTACATGAAGGCTGAATATTTGGTATCCTTCGGCGTGTGGAATGCGG
CACTGACATTTGGAAGGGAGACAGTGCTCGAGTACAAAGCCGCCGCACTACCCTCGGACTTCTTCCCATCGGT
CAAAGCTTACATGGACGATGTAGTCCTCGGCGTTAACTTAGTAGTGGACTTTTCTCAATTTTCCAGAAACGCA
GCGGCCAGATGGATGTGCCTTCGGCGTTTTATAATAAACGCCGCTCGATTCAGCTGGCTATCACTCCTAGTTC
CATTTAATGCAGCTACACCCGCACGGGTGACAGGTGGAGTTTTCAAGGCAGCGTGGCTTTCACTGCTTGTGCC
ATTTGTGAACTCAGCTATTTGCTCAGTAGTGAGAAGGAAGGCAAAATTCGTCGCTGCCTGGACTCTCAAAGCT
GCCGCAAAGTGGATGATGTGGTATTGGGGACCGAGCTTGTACAAAGCGGCCTCTACTCTGCCAGAAACTACCG
TAGTGAGAAGAAAACTGAGCCTGGACGTCAGCGCGGCATTCTACTGA

Figure 22E

HBV-30C

MGMQVQIQSLFLLLLWVPGSRGFLLSLGIHLNAAAKYTSFPWLLNAAARFSWLSLLVPFNAAFPHCLAFSYMK
AALVVDFSQFSRGAILLLCLIFLLNAAAHTLWKAGILYKKAWMMWYWGPSLYKAYPALMPLYACIGAAAWLSL
LVPFVNFLLTRILTINIPIPSSWAFKAAAEYLVSFGVWNLPSDFFPSVKFLPSDFFPSVKDLLDTASALYNSW
PKFAVPNLKAAASAICSVVRRKLSLDVSAAFYNAAAKFVAAWTLKAAAKAANVSIPWTHKGAAGLSRYVARLN
AAASTLPETTVVRRKHPAAMPHLLKAAARWMCLRRFIINASFCGSPYKAAYMDDVVLGVNALWFHISCLTFKA
AATPARVTGGVFKAAALTFGRETVLEYKQAFTFSPTYK

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GTTTTCATGGCTGAGTCTGCTAGTACCTTTCAATGCGGCTTTCCCACATTGCCTAGCTTTTAGCTATATGAAA
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GCCGCCACCCCCGCTCGTGTGACAGGAGGTGTCTTCAAAGCCGCGGCACTGACTTTCGGTCGGGAAACTGTAT
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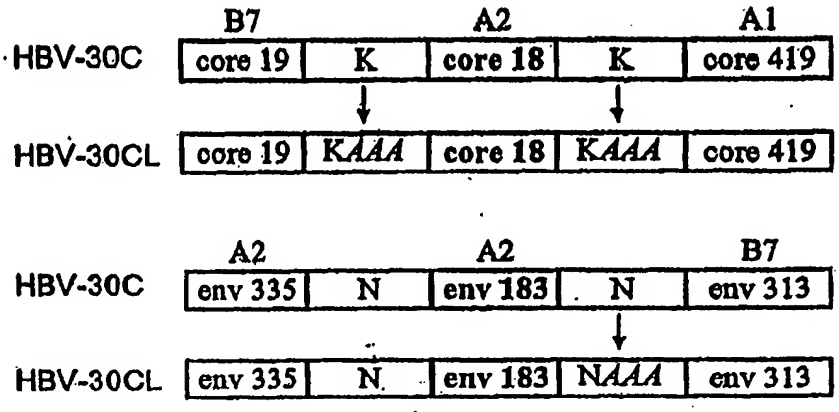
Figure 23A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A2
A1
HBV-30C
core 19
K
core 18
K
core 419
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core 19
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core 18
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core 419
A2
A2
B7
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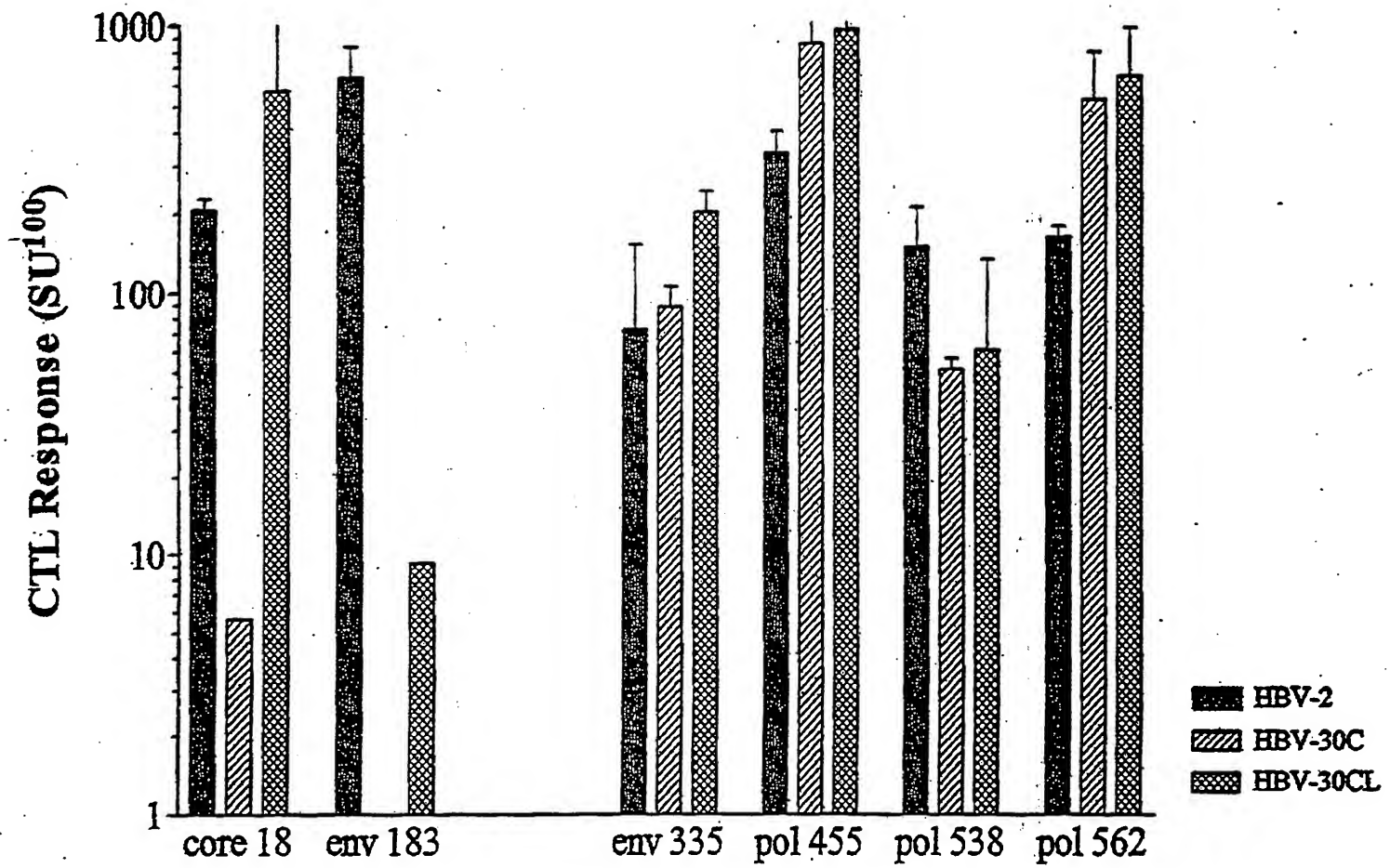
env 313
HBV-30CL
env 335
N
env 183
NAAA
env 313

Figure 23B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100
10
1
CTL Response (SU100)
core 18
env 183
env 335
pol 455
pol 538
pol 562
HBV-2
HBV-30C
HBV-30CL

Figure 23C

HBV-CL

MQVQIQSLFLLLLWVPGSRGFLLSLQIHLNAAAKYTSFPWLLNAAARFSWLSLLVPFNAAFPHCLAFSYMKAA
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PFVNFLLTRILTINAAAIPIPSSWAFKAAAEYLVSFGVWNLPSDFFPSVKAAAFLPSDFFPSVKAAADLLDTA
SALYNSWPKFAVPNLKAAASAICSVVRRKLSLDVSAAFYNAAAKFVAAWTLKAAAKAANVSIPWTHKGAAGLS
RYVARLNAAASTLPSTTVVRRKHPAAMPHLLKAAARWMCLRRFIINASFCGSPYKAAYMDDVVLGVNALWFHI
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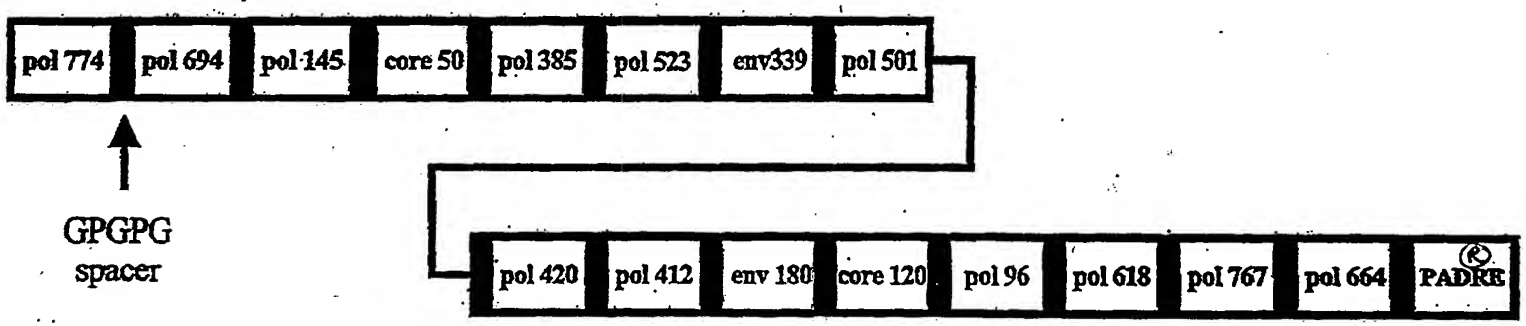
Figure 24A

Supertype	Epitope	SOR # found	HLA-DR Binding Capacity (IC50 nM) DRB1*0101	DRB1*0301	DRB1*0401	DRB1*0404	DRB1*0405	DRB1*1101	DRB1*1201	DRB1*1302	DRB1*0701	DRB1*0802	DRB1*0901	DRB3*0101	DRB3*0151	DRB4*0101
DR	pol 412	10	2.0	21	-	10.0	47	303	397	143	173	606	791	1087	1837	4179
	pol 684	11	10	41	-	88	181	82	-	180	90	416	142	144	4348	322
	env 180	10	1	217	-	9	258	6	4229	9	8	189	55	1158	4374	696
	pol 774	9	15	748	-	119	94	463	-	-	94	818	220	400	-	-
	core 120	8	27	43	-	58	220	11	817	585	78	78	1773	7	8454	396
	pol 145	10	17	4.0	-	2271	1499	42	149	766	61	38	133	35	-	782
	env 239	9	408	14	-	315	28	54	452	2330	2744	60	31	1518	1661	22
	pol 601	6	248	558	-	77	244	492	9452	-	-	800	1531	580	-	102
	pol 825	7	27	359	-	560	248	1749	-	59	328	940	1373	4764	-	1347
	pol 618	6	3.0	4370	-	40	34	1617	-	821	62	872	5175	1248	-	3060
	pol 787	8	55	366	-	966	1634	1520	802	143	44	214	299	3276	-	6553
	core 60	7	810	8.0	-	328	-	458	-	-	678	210	952	124	575	48
DR3	pol 694	2	7470	5009	67	490	1203	-	-	2022	-	-	-	-	1808	1044
	pol 365	3	7372	1368	36	208	291	-	-	948	-	-	-	-	2525	8711
	pol 98	1	8415	4153	43	3916	1908	6666	-	4481	-	5354	-	4330	-	8121
	pol 429	4	38	3089	82	188	17	4923	1859	38	5063	1065	7125	-	6	7

Figure 24B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env339
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spacer
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env 180
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pol 96
pol 618
pol 767
pol 664
PADRE®

Figure 24C

HBV-HTL

MGTSFVYVPSALNPADGPGPGLCQVFADATPTGWGLGPGPGRHYLHTLWKAGILYKGPGPGPHHTALRQAILC
WGELMTLAGPGPGESRLVVDFSQFSRGNGPGPGPFLLAQFTSAICSVVGPGPGLVPFVQWFVGLSPTVGPGPG
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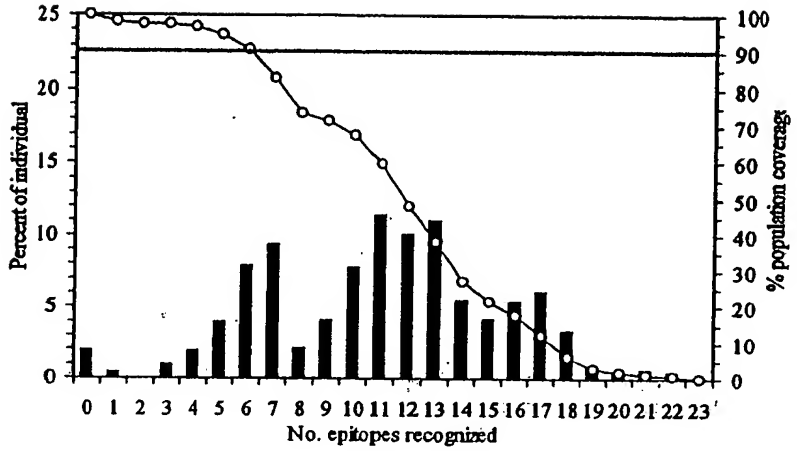
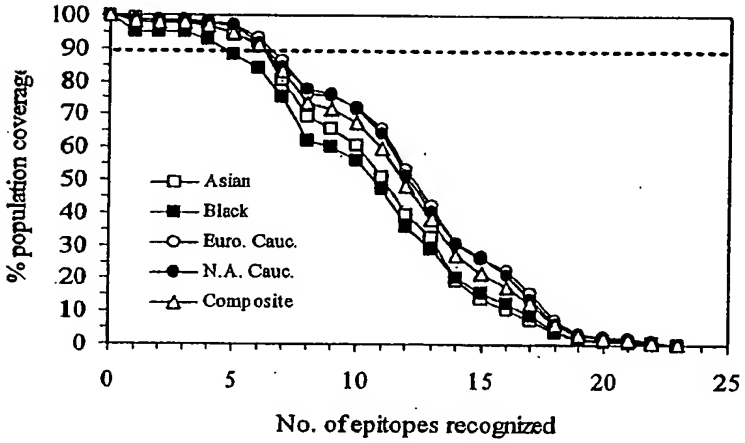
GCAGAGGAAACGGACCCGGCCCTGGGCCTTTTCTGCTGGCTCAGTTTACATCTGCTATTTGTTCTGTGGTCGG
CCCCGGGCCCGGACTCGTGCCTTTCGTGCAGTGGTTCGTGGGACTGTCCCCTACAGTCGGGCCCGGCCCAGGG
CTGCATCTGTACTCCCACCCAATCATCCTCGGCTTCCGCAAGATTGGACCCGGCCCAGGCTCCAGCAATCTCT
CCTGGCTCTCTCTGGACGTGTCTGCCGCCTTTGGCCCTGGACCAGGCCTGCAAAGCCTGACTAATCTGCTCAG
CAGCAACCTGTCCTGGCTGGGACCTGGCCCAGGGGCTGGCTTCTTTCTGCTCACCCGGATTCTCACAATTCCC
CAGTCCGGACCAGGACCAGGAGTCAGTTTCGGGGTGTGGATCAGGACCCCTCCTGCTTATAGACCACCCAATG
CTCCAATCGGCCCCGGCCCTGGCGTCGGGCCACTGACCGTGAATGAGAAGCGCCGGCTGAAGCTGATCGGCCC
TGGCCCTGGCAAGCAGTGCTTTCGCAAACTGCCCGTGAACAGACCTATTGATTGGGGCCCCGGCCCTGGAGCA
GCCAACTGGATTCTCAGGGGAACAAGCTTCGTCTACGTGCCCGGGCCCGGACCAGGGAAGCAGGCTTTTACCT
TCTCTCCCACTTACAAGGCCTTCCTCTGTGGGCCAGGCCCCGGCGCCAAGTTTGTGGCAGCATGGACCCTCAA
AGCCGCTGCCTGA

A.

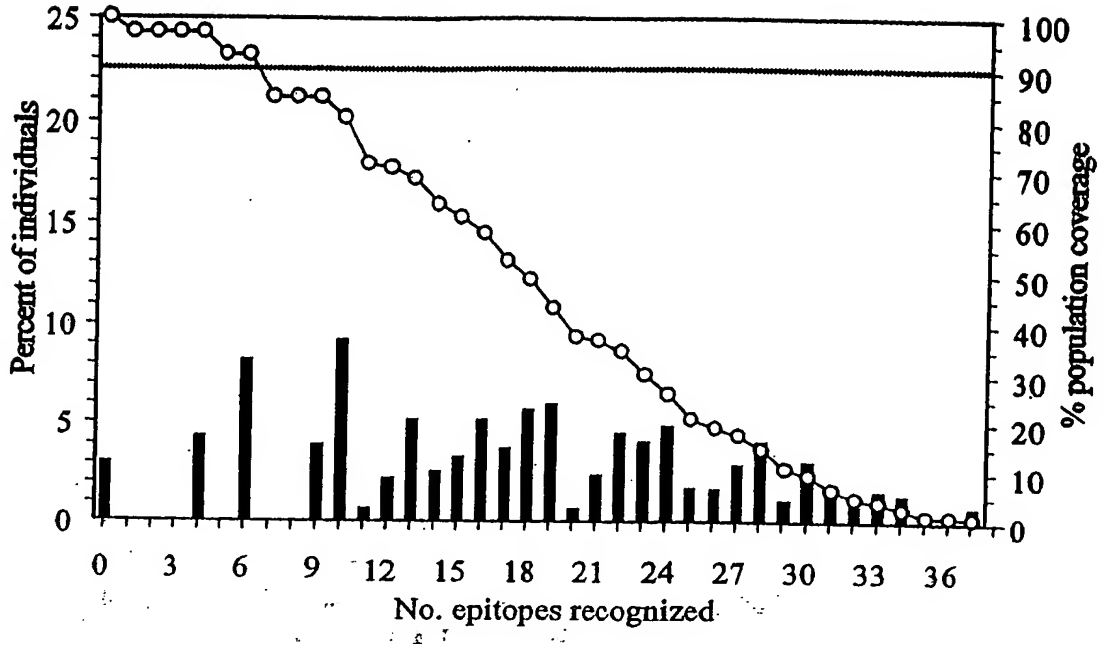


B.

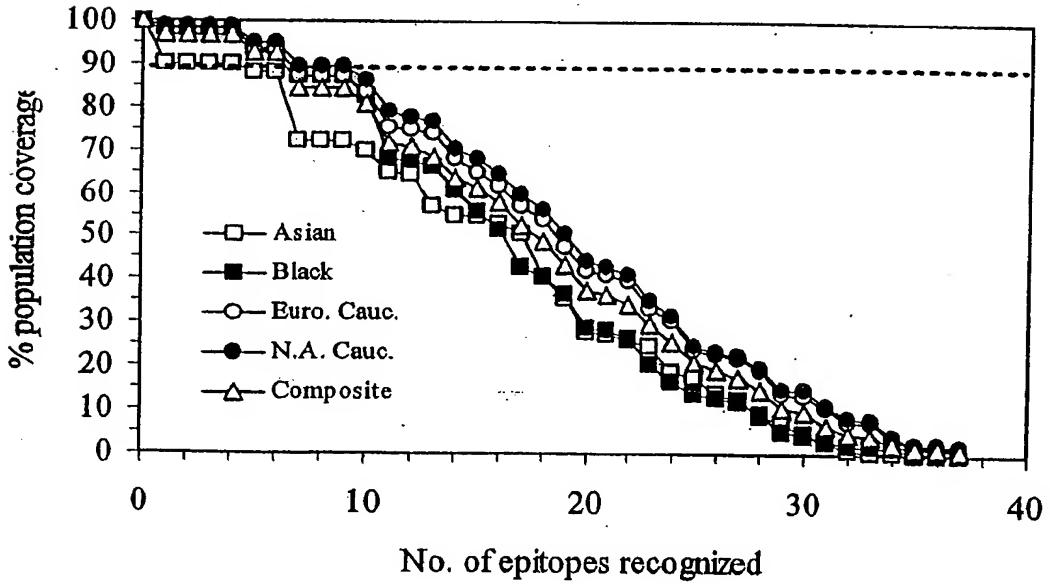


Figures 25A-B

A.

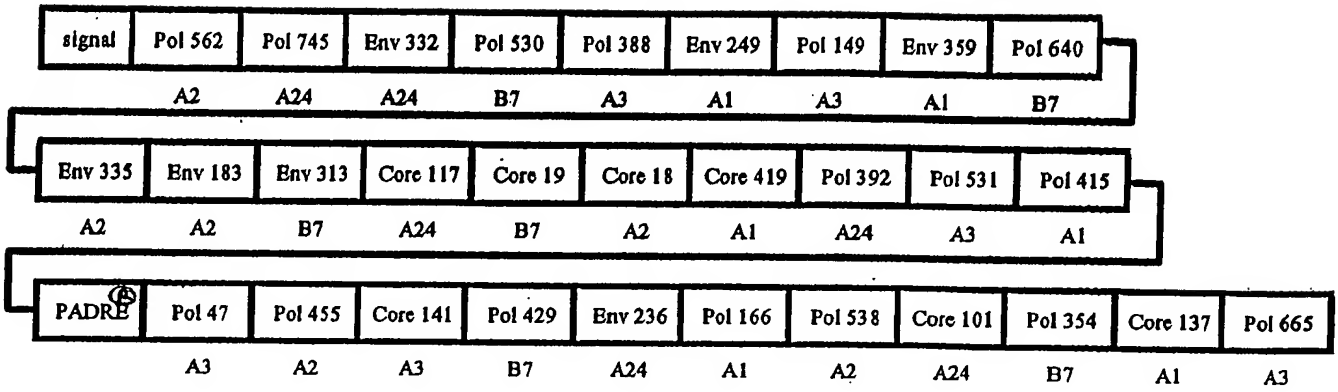


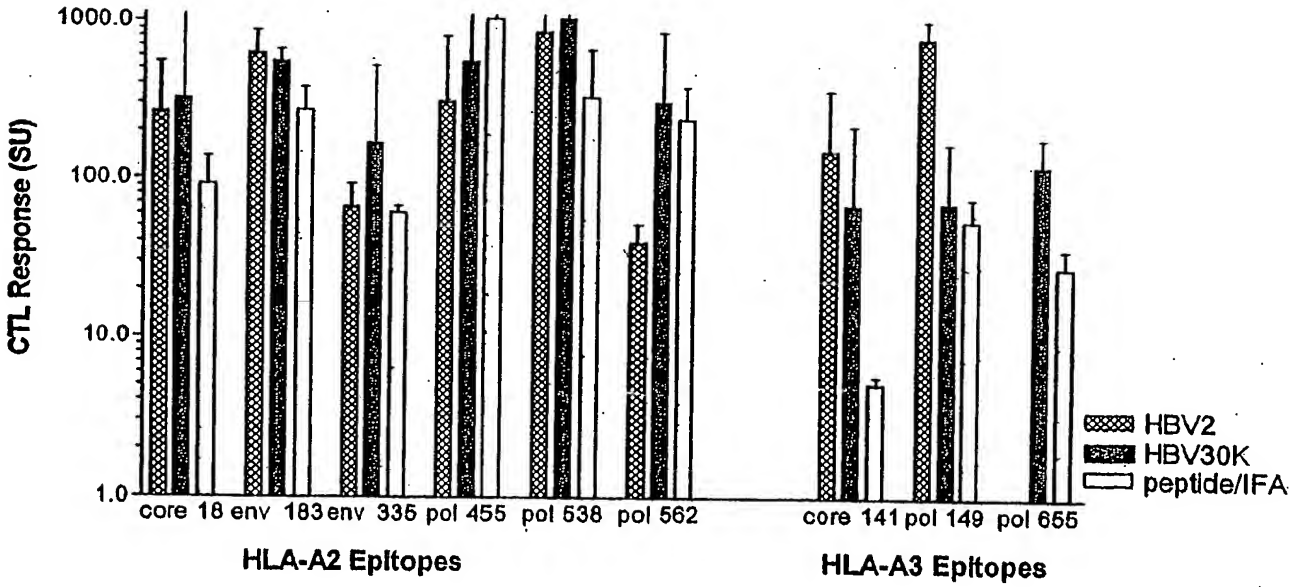
B.



Figures 26A-B

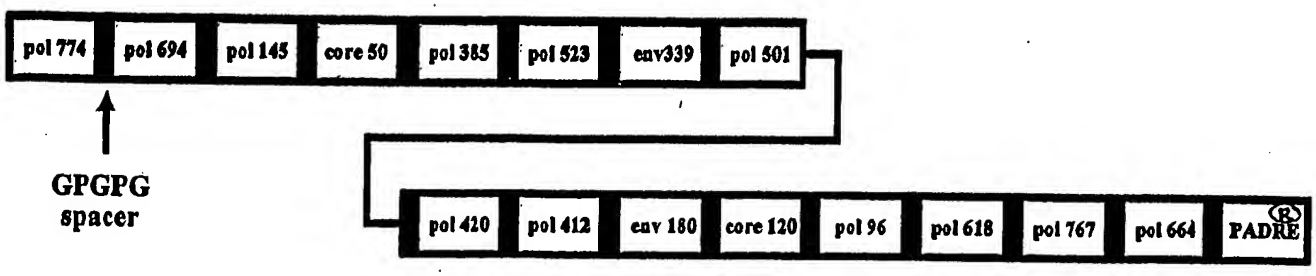
A.



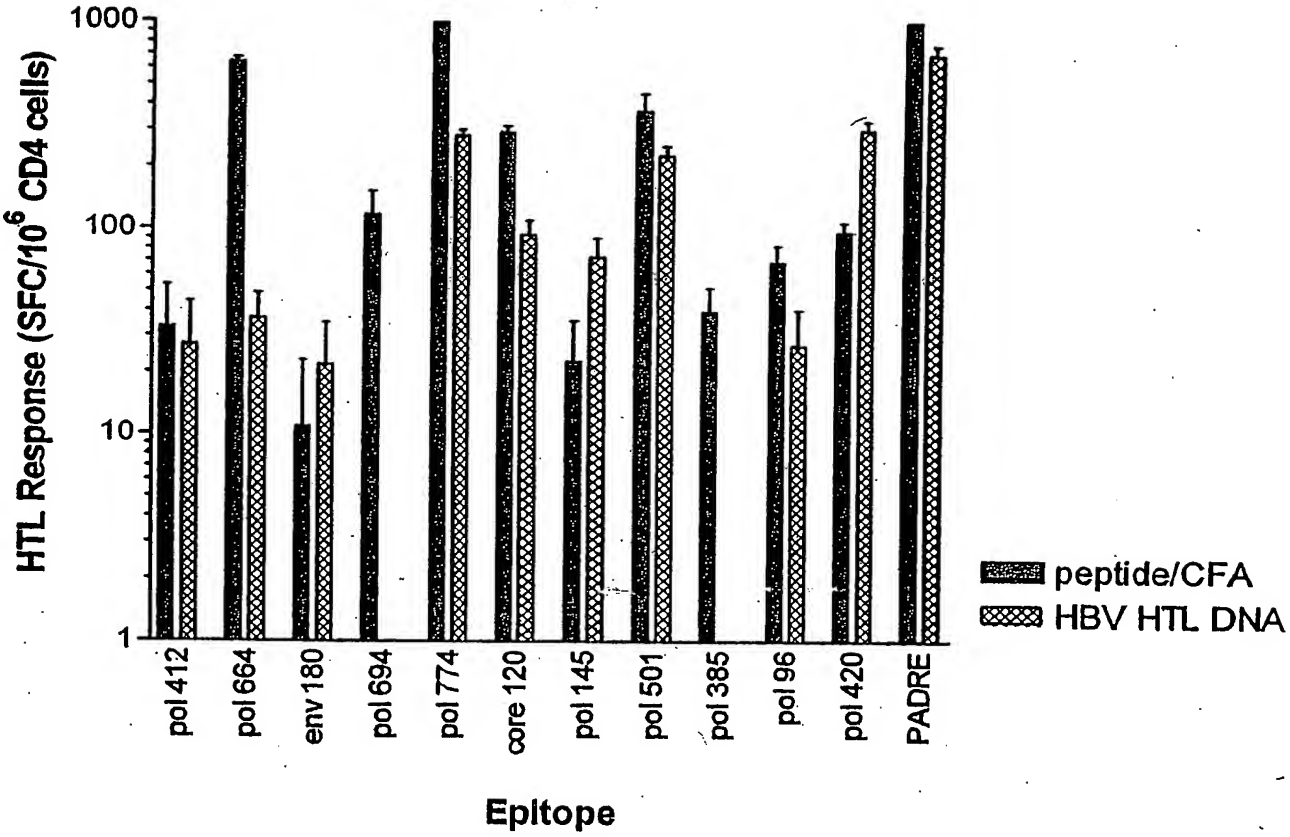


Figures 27A-B

A.

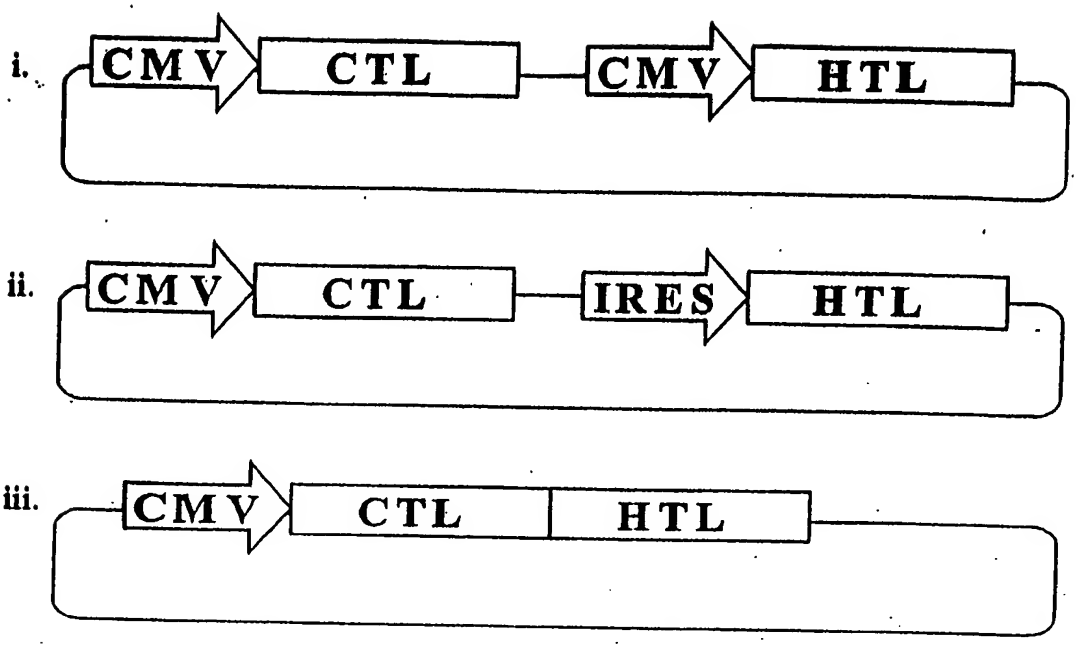


B.

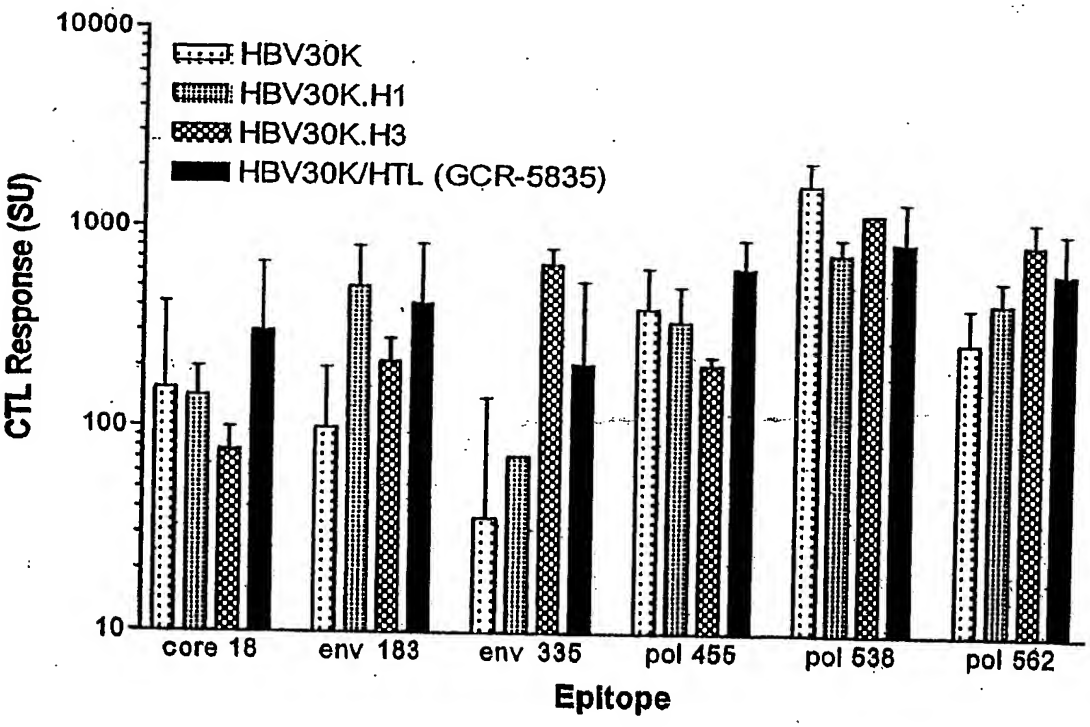


Figures 28A-B

A.



B.



Figures 29A-B

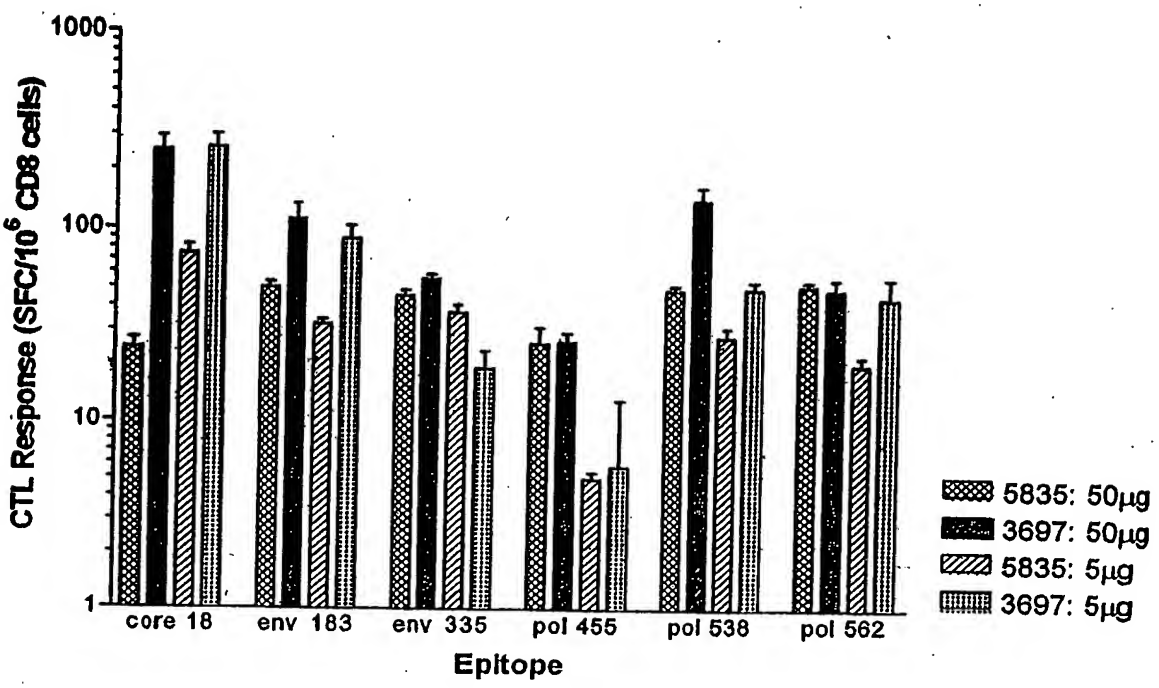

1000
100
10
1
CTL Response (SFC/10^6 CD8 cells)
core 18
env 183
env 335
pol 455
pol 538
pol 562
Epitope
5835: 50µg
3697: 50µg
5835: 5µg
3697: 5µg

Figure 30

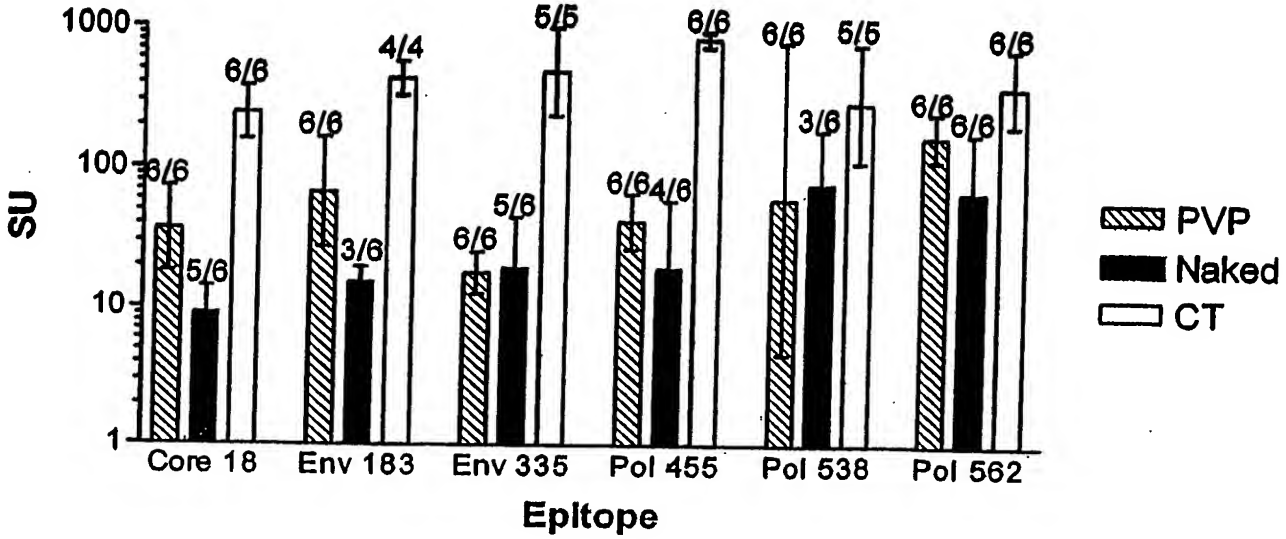
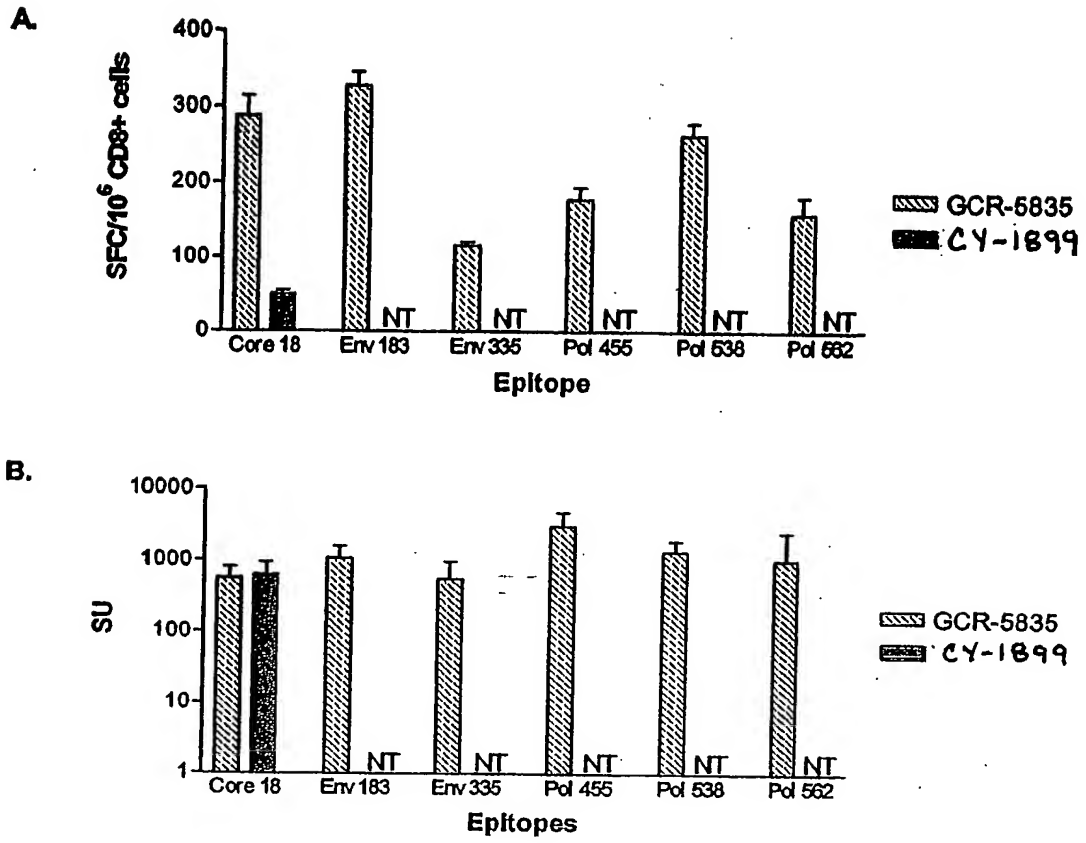
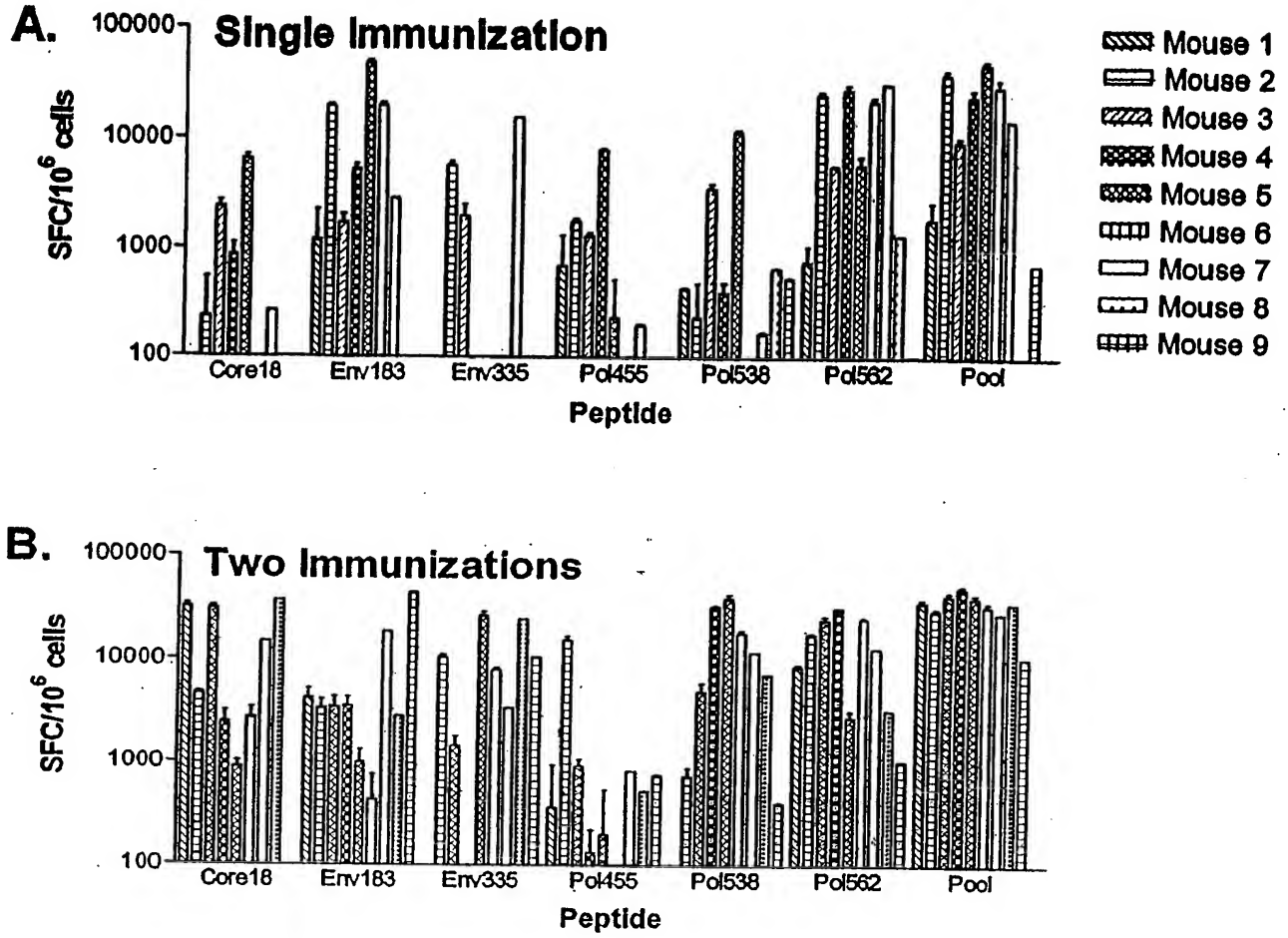

1000
100
10
1
SU
6/6
5/6
6/6
6/6
3/6
4/4
6/6
5/6
5/5
6/6
4/6
6/6
6/6
3/6
5/5
6/6
6/6
6/6
Core 18
Env 183
Env 335
Pol 455
Pol 538
Pol 562
Epitope
PVP
Naked
CT

Figure 31



Figures 32A-B



Figures 33A-B

Composition of HBV poly-epitope vaccine

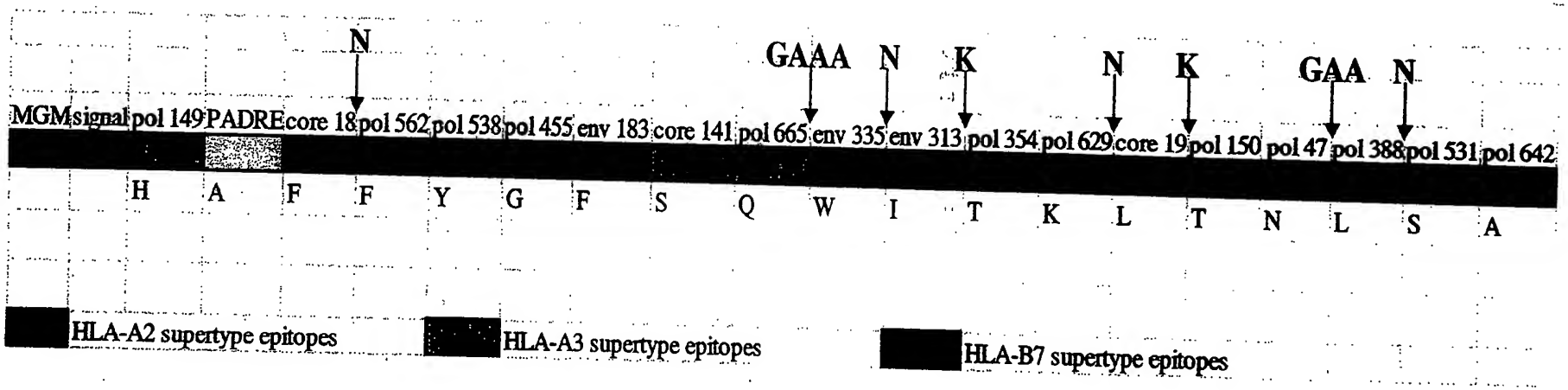


FIG. 34

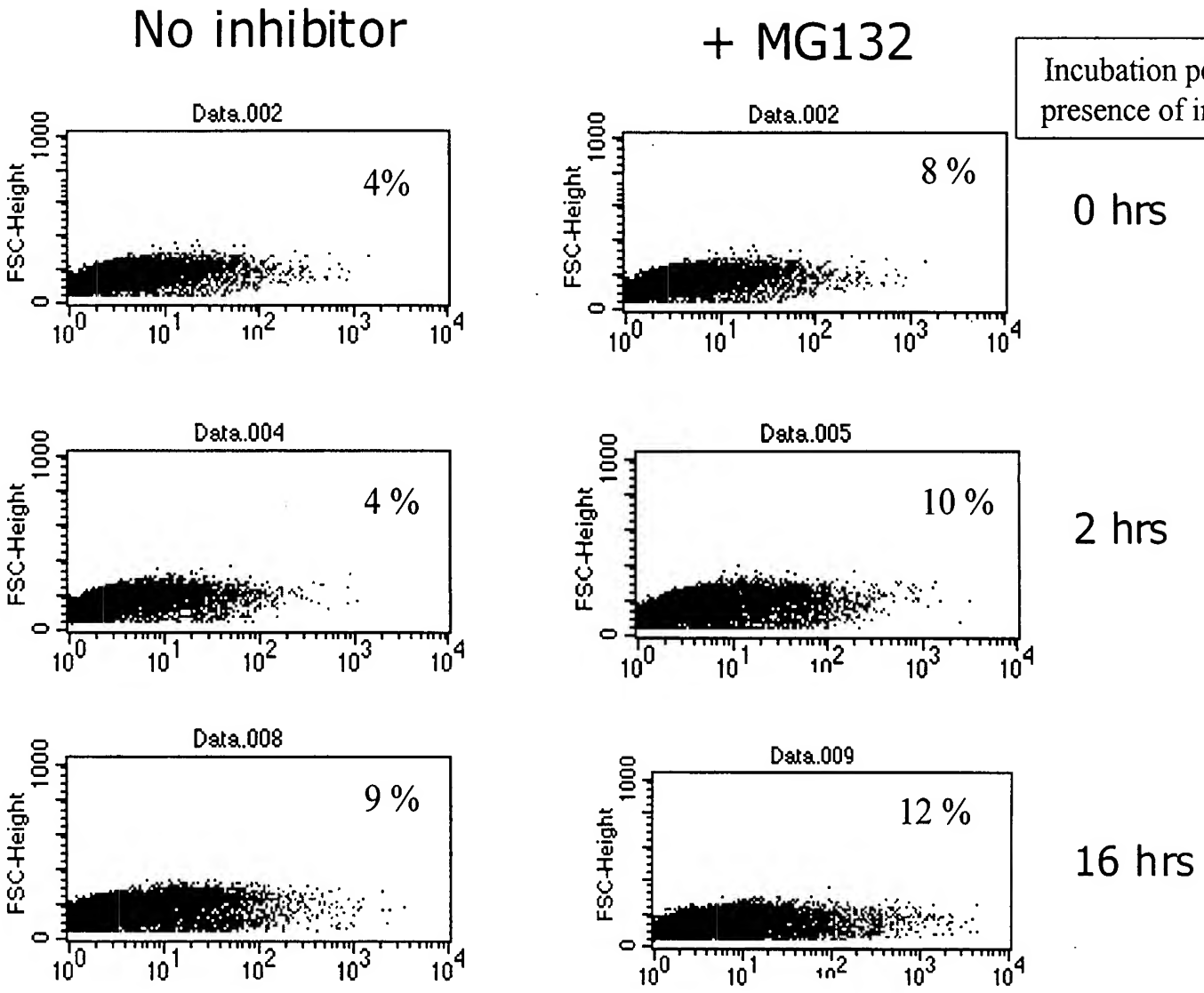
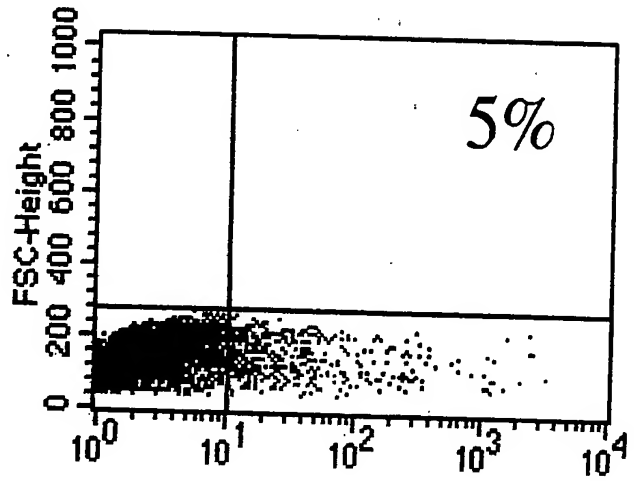

No inhibitor
+ MG132
Incubation period in presence of inhibitor
Data.002
4%
Data.002
8 %
0 hrs
Data.004
4 %
Data.005
10 %
2 hrs
Data.008
9 %
Data.009
12 %
16 hrs
FSC-Height
1000
0
10^0
10^1
10^2
10^3
10^4

FIG. 35 A

Detection of HBV AOSIb (un-optimized epitope string)

- MG132



+ MG132

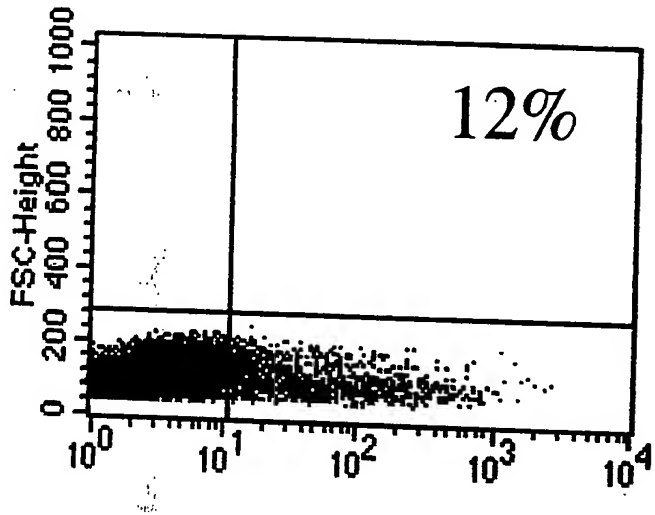


FIG. 35B

Detection of HBV AOSIb2 (processing optimized epitope string)

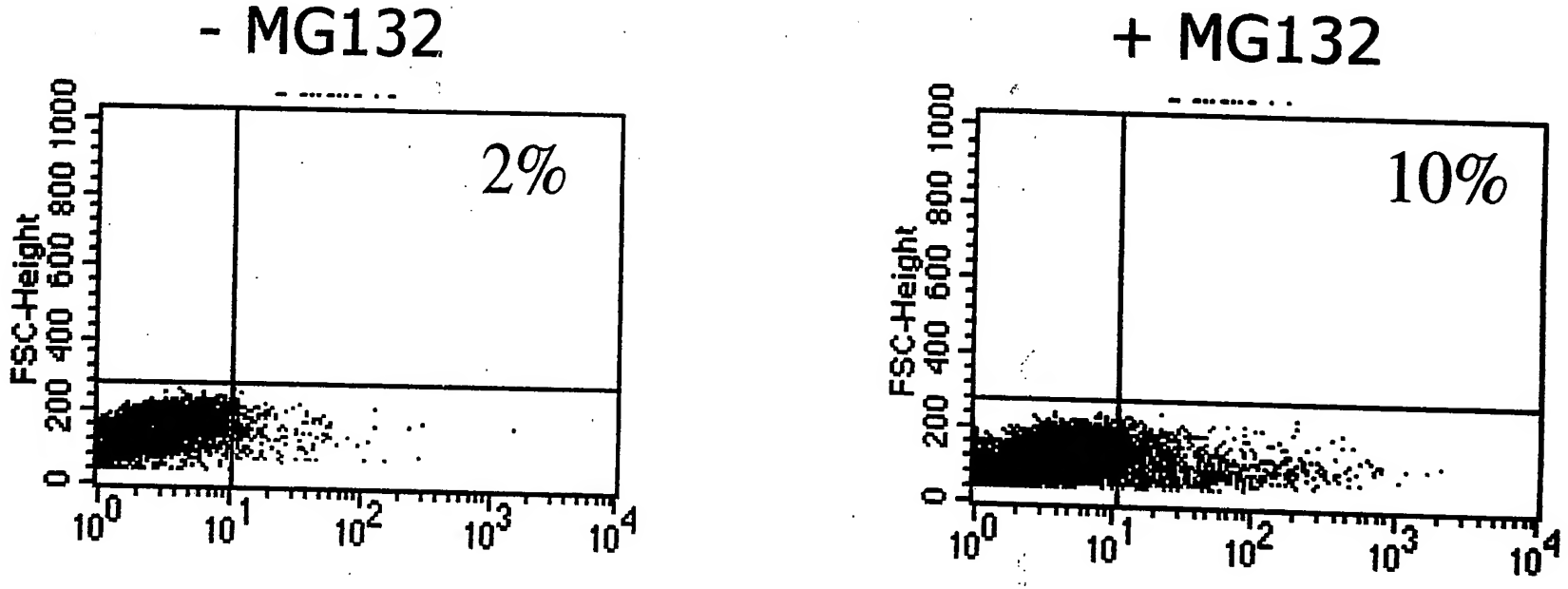


FIG. 35C

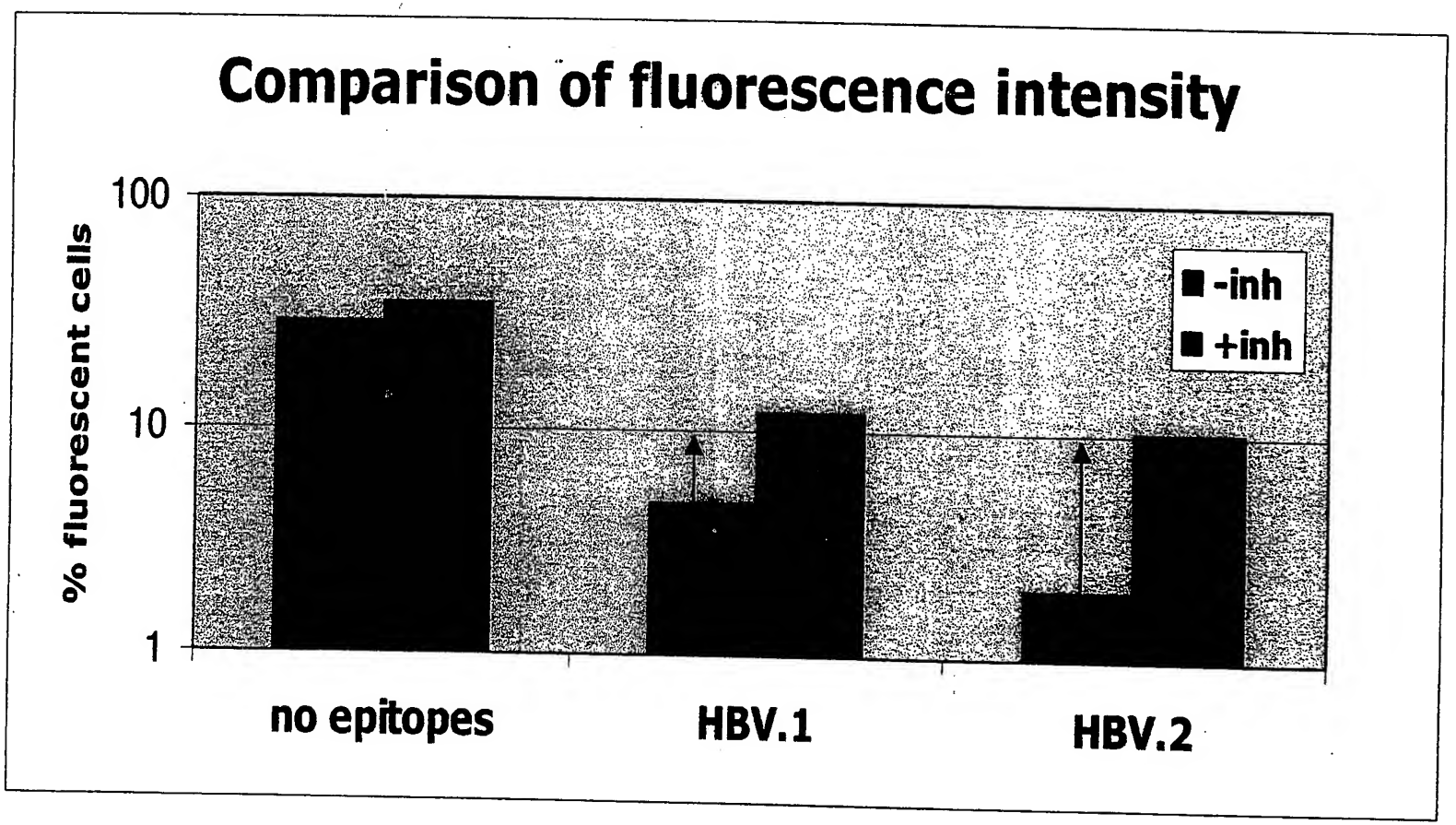


FIG. 35D

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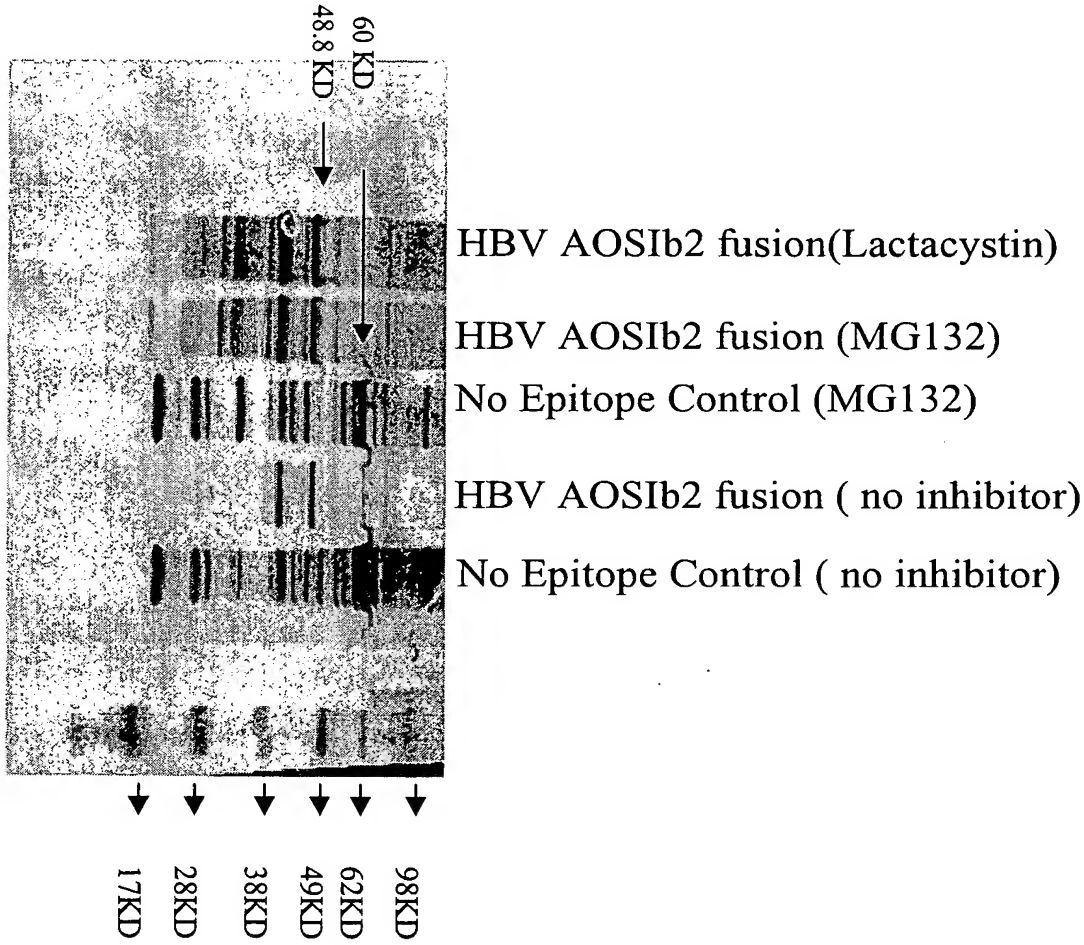
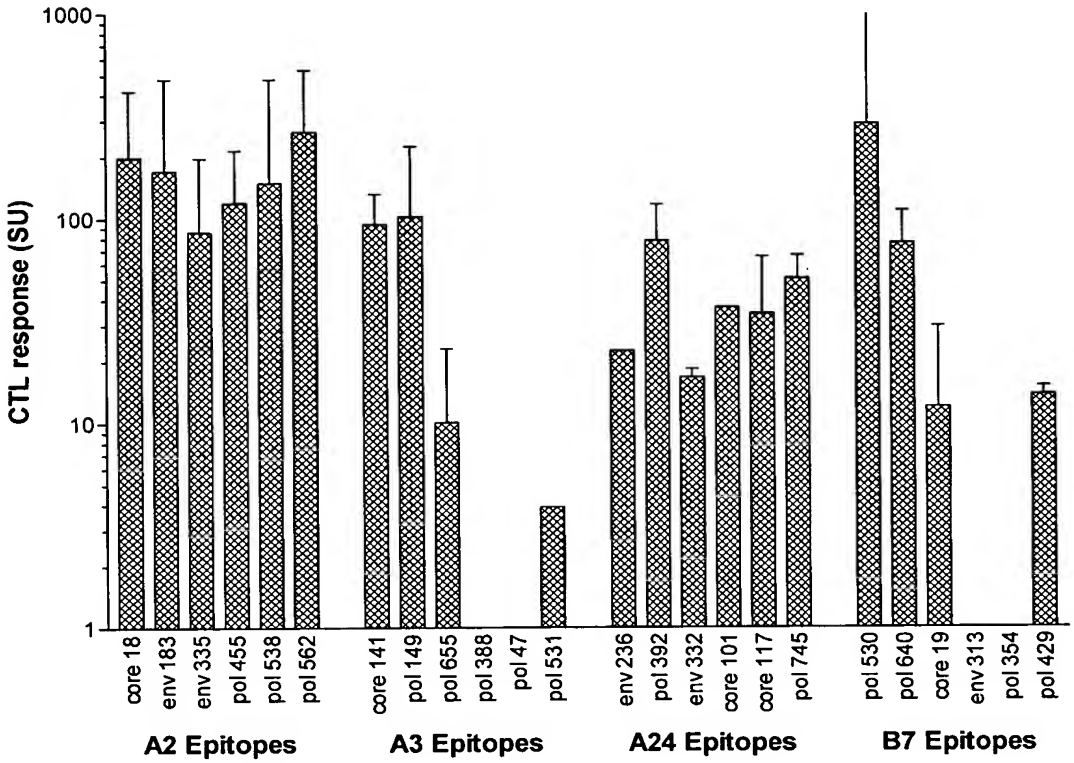
plasmid	No inhibitor	with inhibitor	Fold Increase (aver.)
Fluorescent Protein (no epitopes control)	30% 34%	35% 33%	1.1
HBV AOSIb fusion	5% 4.4	12% 8%	2.1
HBV AOSIb2 fusion	2% 1.2%	10% 6.6	5.3

FIG. 35E

FIG. 36


48.8 KD
60 KD
HBV AOSIb2 fusion(Lactacystin)
HBV AOSIb2 fusion (MG132)
No Epitope Control (MG132)
HBV AOSIb2 fusion (no inhibitor)
No Epitope Control (no inhibitor)
17KD
28KD
38KD
49KD
62KD
98KD



GCR-3697 Immunogenicity Data

HLA Supertype	Epitope	CTL response (SU) 2 x PVP Immunization Freq.	GeoMean	X/+	CT Pre-treatment Freq.	GeoMean	X/+
HLA-A2	core 18	12/12	199.3	2.1	4/4	288.9	1.3
	env 183	12/12	171.2	2.8	4/4	401.2	1.4
	env 335	12/12	86.4	2.3	4/4	153.6	1.7
	pol 455	12/12	120.4	1.8	4/4	411.3	1.8
	pol 538	12/12	149.9	3.2	4/4	148.1	2.2
	pol 562	12/12	266.2	2	4/4	353.3	1.5
HLA-A3	core 141	6/6	94.4	1.4	12/12	167.6	1.4
	pol 149	6/6	103	2.2	12/12	386.7	1.5
	pol 655	5/6	10.1	2.3	12/12	108	3.6
	pol 388	0/6			0/12		
	pol 47	0/6			3/12	3.2	1.1
	pol 531	1/6	3.9		2/12	5.5	1
HLA-A24	env 236	1/6	22.6		2/11	23.4	1.2
	pol 392	5/6	78.1	1.5	10/11	54.8	2.2
	env 332	2/6	16.7	1.1	3/11	25.6	1.6
	core 101	1/6	37		0/11		
	core 117	3/6	34.4	1.9	2/11	27.4	3
	pol 745	2/6	51.2	1.3	1/11	32.6	
HLA-B7	pol 530	6/6	292.4	3.1	3/6	177	1.3
	pol 640	4/6	76.5	1.7	5/7	104.6	1.8
	core 19	3/6	12	2.5	2/7	8.8	1.6
	env 313	0/6	0	0	6/6	323.1	2.9
	pol 354	0/6	0	0	4/6	351.5	3.2
	pol 429	2/6	13.7	1.1	1/6	1.4	

FIGURES 37A-37B

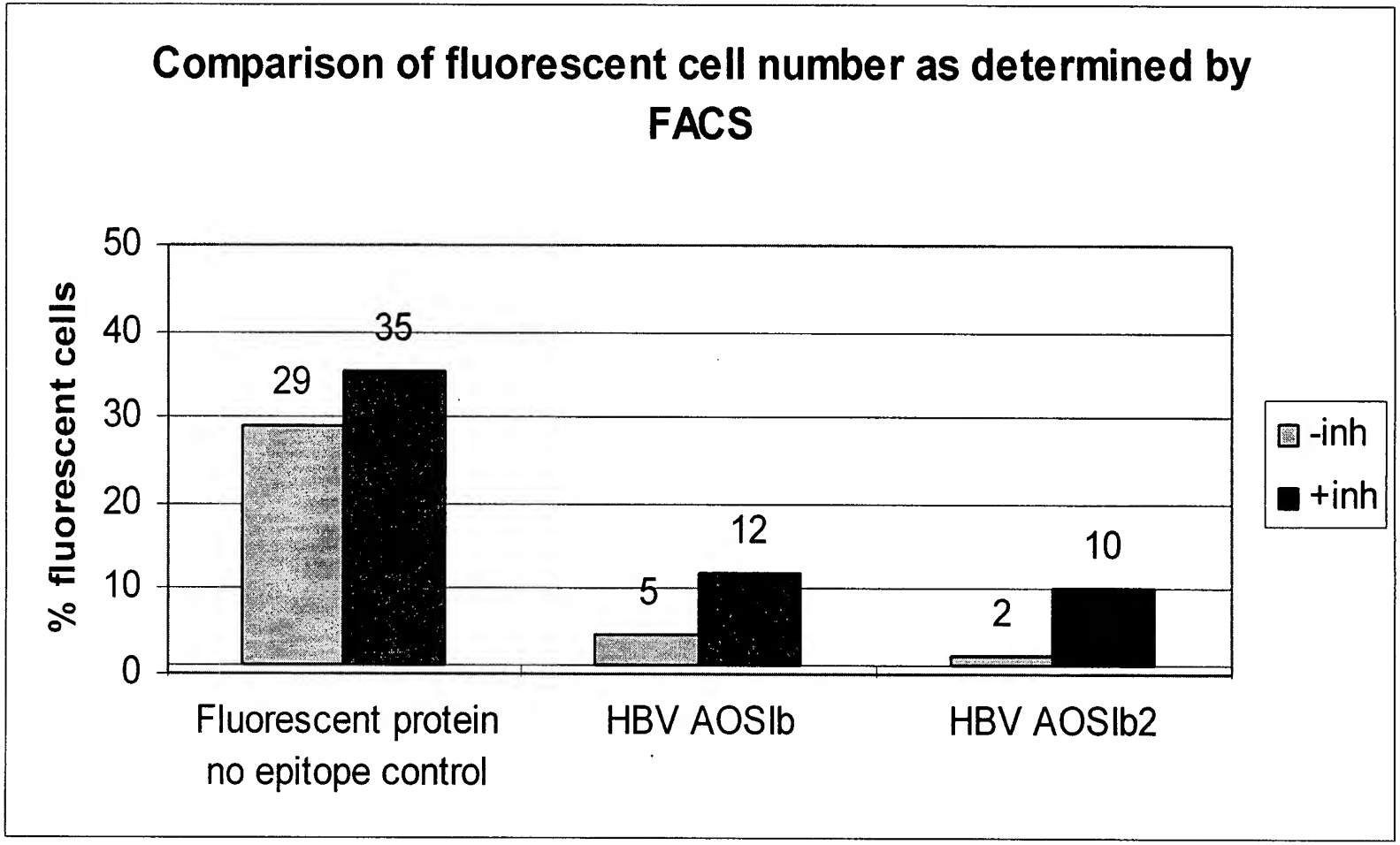

Comparison of fluorescent cell number as determined by FACS
% fluorescent cells
50
40
30
20
10
0
29
35
5
12
2
10
-inh
+inh
Fluorescent protein no epitope control
HBV AOSIb
HBV AOSIb2

FIG. 38

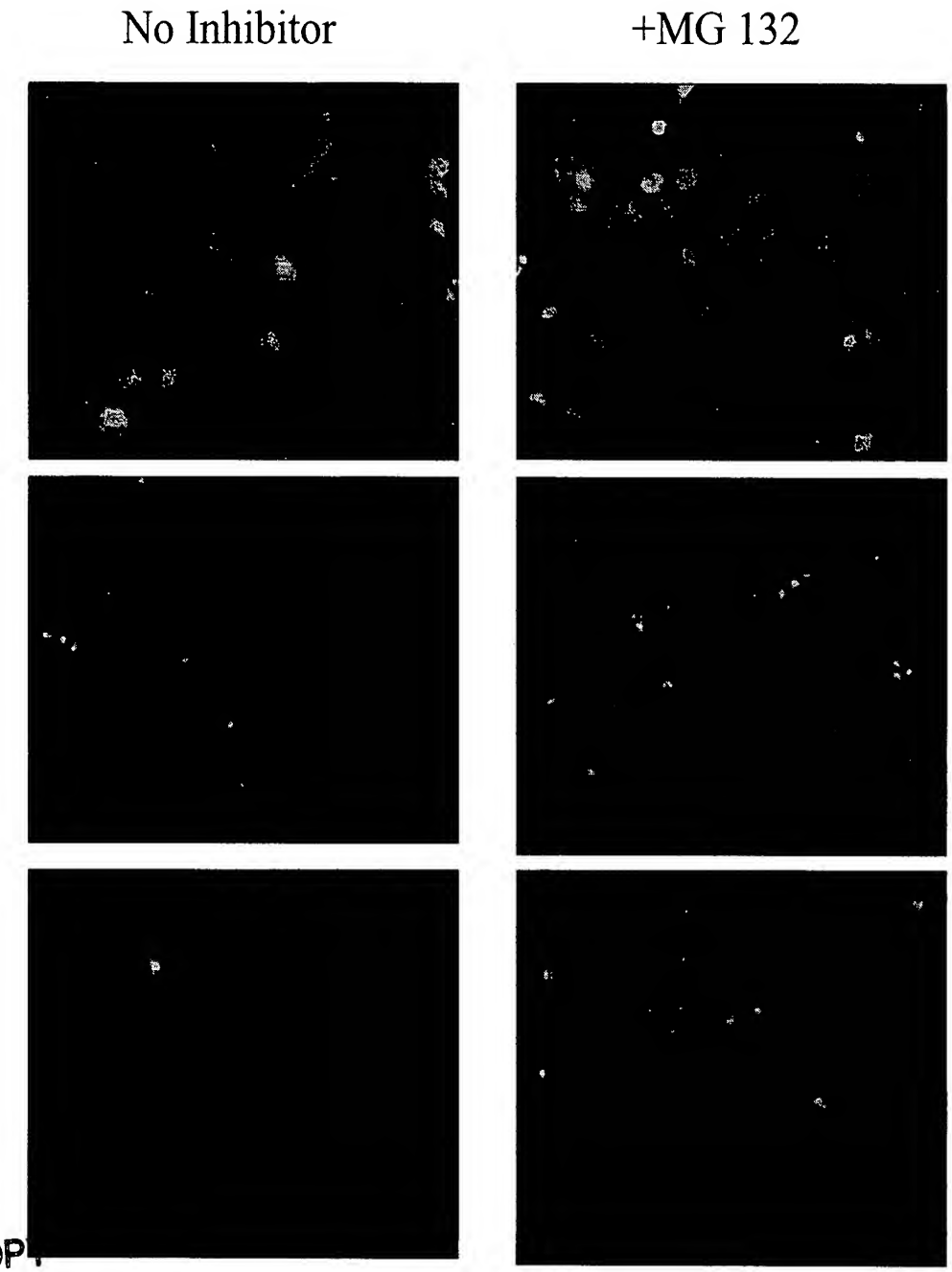


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FIG. 39